

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

ATGCCAAGCC	GSTGCTGATG	CCCGAGCTCG	GCGAATCGGT	GACCGAGGGG	ACCGTCATTC	60
GTGGGCTGAA	GAAGATCGGG	GATTCGGTTC	AGGTTGACGA	GCCACTCGTG	GAGGTTCCCA	120
CCGACACAGOT	GGACACCGAG	ATCCCGTCCC	CGGTGGCTGG	GGTCTTGGTC	AGTATCAGCG	180
CCGACGAGGA	CGCCACGGTG	CCCGTGGGCG	GCGAGTTGCG	CCGGATCGGT	GTGCTGCCCG	240
AGATCGGCGC	CGCGCCGCC	CCCAAGCCCC	C			271

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Ala	Lys	Pro	Val	Leu	Met	Pro	Glu	Leu	Gly	Glu	Ser	Val	Thr	Glu	Gly	
1				5					10					15		
Thr	Val	Ile	Arg	Trp	Leu	Lys	Lys	Ile	Gly	Asp	Ser	Val	Gln	Val	Asp	
			20					25					30			
Glu	Pro	Leu	Val	Glu	Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	Pro	
			35				40						45			
Ser	Pro	Val	Ala	Gly	Val	Leu	Val	Ser	Ile	Ser	Ala	Asp	Glu	Asp	Ala	
			50				55				60					
Thr	Val	Pro	Val	Gly	Gly	Glu	Leu	Ala	Arg	Ile	Gly	Val	Ala	Ala	Glu	
			65			70			75					80		
Ile	Gly	Ala	Ala	Pro	Ala	Pro	Lys	Pro								
							85									

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAGGTAGCGG	ATGSCCGGAG	GAGCACCCCA	GGACCCGCCC	CGAACCCGCG	GTCCCGGTCA	60
TGATATGTG	GGCACCGTTC	GTCCCTCCCG	CCGAGGTGAT	TGACGAT		107

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATGAAGTTGA AGTTTGCTCG CCGAGTACT GCGATACTGG GTTGTCAGC GGCCTTTGTG	60
TTTCTGCTCT CGGTTGGCCAG CGCAGATCCA CCGACCCGCG ATCAGCCGGA CATGACGAAA	120
GACTATTGCC CGGGTGGCCG ATGGGGTTTT GCGACTTTGG CCGTGTGCGA CGCGAGAGAAG	180
TACCCGAGCG GCTCGTTTTG GCACCAATGG ATGCAAACGT GGTTTACCGG CCGACAGTTT	240
TACTTCGATT GTGTCAGCGG CGGTGAGCCG CTCCCGCGCC CGCCGCCACC GGGTGGTTGC	300
GGTGGGCGCA TTCCCTCCGA GCAGCCCAAC GCTCCCTGA	339

(i) INFORMATION FOR SEQ ID NO:241:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala	
1 5 10 15	
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp	
20 25 30	
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp	
35 40 45	
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly	
50 55 60	
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe	
65 70 75 80	
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro	
85 90 95	
Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro	
100 105 110	

(i) INFORMATION FOR SEQ ID NO:242:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GTGACCACGG	TGGGCTGCC	ACCAACCTGG	GCACGGGCG	CGCGCGGGC	GCGGGGGCT	50
CCGGCGGCAA	CGGTGGGCC	GGGGTAAAG	CCACGGGCTC	AGGCGGCAAG	GGCGGGGGCG	120
GTGGCAATGG	CGGTGATGGG	AGCTTCGGCG	CTACGAGCGG	CGCCGCTCC	ATCGGGGTGA	180
CGGGGGGGCG	CGCGGGCAAC	GGCGGCAAGG	GGCGGGCGCG	TGGCAGGAC	CCCAACGGCT	240
CAGGTGGCGA	CGCGGGCAAA	GGCGGCAAGG	GCCTGTGCGG	CGGCAACGGG	GGCTCGATCG	300
GCGCCAACAG	CGCATCGCTC	GGCGGTTCGG	GTGGGGCGGG	TGGCGCTGCG	GGCGCGGGCG	360
GAAACGGCAG	C					371

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GTCCGGGTCC	CACCACCGCG	CGCGCGGGCG	CTTACGGGCG	GGCGGACCA	GCGGCTTTTC	60
TTGACTCGTT	CRAGAAAAGG	GCCTTCCTTT	TGGTGGGCA	TGTTGGCATG	ATCGTGACCC	120
ATGGGCAACA	TCGACGTCCA	CATCTCGGCG	AAGGTCTAGC	TCCATGCGAA	TGGCGCGCGC	180
GGTGGTGAGC	ATCGGTCTAG	CGCTCATAGC	AGGGTTGCGG	GTACCTGTTG	CGGACGCACA	240
CCCGTGGGAG	CGCGGGGTGG	TGTCTACGCG	GTTGCTCGGA	AAGGGGTGCG	TGGGCAACAT	300
CGTGGGCGCC	CGAATGGGGT	GGGAGGCGGT	GTTCAACCAAG	CGGTTCCAGG	CGTTTGGGGT	360
CGAATACCG	CGCTGCAACA	ATGCGGTGGA	CATCGGGCTG	CGCGAGGTGT	ACGACCATCC	420
CGAC						424

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GGCATGCGCG	CGCGGGGTAC	CACCGGCAAT	GTGGAAAGGT	TTCCCAACCG	CAACGATGCT	60
TTGCATCTGG	CTCAATTGGA	CTTCAGCGCG	GCCGATTTCG	TCACCGAGGG	CCACGGTCTA	120
AGGGCGGATG	CGATCTTACT	CGGCGGTACC	GACCGGCTGC	CTTTGCGCGA	GGCGCGGGAT	180
TGGGACTTGG	TGGAGTGGCA	GTTCGCGAGC	ACCGTCACCG	CGGACACGGT	GGCATCGAC	240
GTATCGCGCG	ACGATATGCG	TCCCGAACTG	GGCGGGGGCT	CCAACTGAC	CGAATGCTTG	300
CGGCTCTACG	ATTGCTC					317

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TGGGGTATGC	GCTTCGCAGC	CGGTGCGCGG	TCAACGCGCC	GGAGGCAATC	GCTTCGCTGC	60
CGAGGAATGG	TTGATCTACG	ATCGCAGTGT	GCGGTCTGTG	ACCGACACCG	CGGTCCCAACG	120
TGAAGTGAAG	GGGAAAATC	GGCGAAATC	TGCGCTCTAG	TTACAGCTCG	GCGCTTAACG	180
GTTCGGGAAG	TTGGGTGCGC	GCTTCCTGGG	GAACGCGCGC	GGGCTTCTCT	TGGCGTCTGC	240
GGACAGGAAG	ACCTTGATGC	CGATCTGGGT	GTCGATCTTG	AACGCTCTGT	TTTCGGGCAT	300
GCATCTGGTC	TGCGCGATGG	ACCGCAAGAT	GGCGTGCACG	GGCAGGGGTC	CGTTAGCCGA	360
GATGGCGTCT	GCAAGTTCTA	GAACCTTGAT	CAACGCGCTG	CGGTGCGGCA	CACGTGCGCG	420
AT						422

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GGGTGCGGCT	GAACACGAGC	CGCGGCGTGC	CAGATCTCCC	GGACTCGGTA	GTGCGGCGCG	60
TGGCGTGGTT	GCTCTCTGTA	CGCGGCGCGG	CGACCATAGG	GTGCTAATG	CGCAGGTAGC	120
GGCGGAGGTG	CATGGAGTCG	ATGATGATGC	GACTCTCCAG	GTGCGCGACC	GGGAGCTTGG	180
CATCGGSCCT	GATCAGCCAG	GACGCGTAGG	ACAACTCGAT	CGAATGCATA	GTGCGCTCCA	240
GATGCGCGGT	GCCACTTCCG	GCGTGCCTCA	CGGCAAAATG	CTTGATTTCT	AGCTCCGCGT	300
AGTGTCTTCC	CATCGCGTGC	GGGATGAATG	GGAAACGCGC	GATGCGGACA	AACGGGTCTG	360
ACCTCAGGTT	TGGCGCTTTG	CGCACAGTGG	TGCACAGCGG	GTACTCGGCA	TAAATGCTGG	420
CCCCCA						426

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

AGACGGGCGA	GGGTGTGCTC	GCTGCGGCGG	GCATTGTGGA	TAATCTGCGC	TGGGTGAGCG	60
CCCGGATGGA	CTAGTGAGGC	GCAACGCTAG	GCTTTGGGAT	ACCCACAGCT	AAAAAGTTTA	120
TCAAAGAAAC	GAAGAAGGTT	GCCATGAGCA	CTGTTGCGCG	CTACGCGCGC	ATGTGCGGGA	180
CCGAACCGCT	GACCAAGACT	ACGATCACCT	GTGCGGACCC	GGGCGCGCAC	GACATGGCGA	240
TGGACATCAA	ATTGCGCGGA	ATCTGTGCGT	CGGACATCCA	TACCTGTCAA	ACCGAATGGG	300
GGCAACCGAA	TTTACTGTGT	GTCTCTG				327

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

Asp His Gly Gly Pro Ala Thr Asn Pro Gly Ser Gly Ser Arg Gly Gly
 1           5           10           15
Ala Gly Gly Ser Gly Gly Asn Gly Gly Ala Gly Gly Asn Ala Thr Gly
 20           25           30
Ser Gly Gly Lys Gly Gly Ala Gly Gly Asn Gly Gly Asp Gly Ser Phe
 35           40           45
Gly Ala Thr Ser Gly Pro Ala Ser Ile Gly Val Thr Gly Ala Pro Gly
 50           55           60
Gly Asn Gly Gly Lys Gly Gly Ala Gly Gly Ser Asn Pro Asn Gly Ser
 65           70           75           80
Gly Gly Asp Gly Gly Lys Gly Gly Asn Gly Gly Ala Gly Gly Asn Gly
 85           90           95
Gly Ser Ile Gly Ala Asn Ser Gly Ile Val Gly Gly Ser Gly Gly Ala
100           105           110
Gly Gly Ala Gly Gly Ala Gly Gly Asn Gly Ser
115           120

```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

Met Ala Ala Ala Gly Thr Thr Ala Asn Val Glu Arg Phe Pro Asn Pro
 1           5           10           15
Asn Asp Pro Leu His Leu Ala Ser Ile Asp Phe Ser Pro Ala Asp Phe
 20           25           30
Val Thr Glu Gly His Arg Leu Arg Ala Asp Ala Ile Leu Leu Arg Arg
 35           40           45
Thr Asp Arg Leu Pro Phe Ala Glu Pro Pro Asp Trp Asp Leu Val Glu
 50           55           60
Ser Gln Leu Arg Thr Thr Val Thr Ala Asp Thr Val Arg Ile Asp Val
 65           70           75           80
Ile Ala Asp Asp Met Arg Pro Glu Leu Ala Ala Ala Ser Lys Leu Thr
 85           90           95
Glu Ser Leu Arg Leu Tyr Asp Ser
100

```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Ala	Tyr	Ala	Leu	Arg	Ser	Arg	Cys	Arg	Val	Asn	Ala	Pro	Glu	Ala	Ile
1				5				10					15		
Ala	Ser	Leu	Pro	Arg	Asn	Gly	Ser	Ile	Thr	Ile	Ala	Val	Cys	Arg	Arg
		20					25					30			
Ala	Pro	Thr	Pro	Pro	Ser	Asn	Val	Asn							
	35					40									

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Val	Pro	Leu	Asn	Thr	Ser	Pro	Arg	Leu	Pro	Asp	Leu	Pro	Asp	Ser	Val
1				5				10					15		
Val	Pro	Pro	Val	Ala	Ser	Leu	Leu	Ser							
		20					25								

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Met	Ser	Thr	Val	Ala	Ala	Tyr	Ala	Ala	Met	Ser	Ala	Thr	Glu	Pro	Leu
1				5				10					15		
Thr	Lys	Thr	Thr	Ile	Thr	Arg	Arg	Asp	Pro	Gly	Pro	His	Asp	Met	Ala
		20					25					30			
Ile	Asp	Ile	Lys	Phe	Ala	Gly	Ile	Cys	Arg	Ser	Asp	Ile	His	Thr	Val
	35					40					45				

Gln Thr Glu Trp Gly Gln Pro Asn Leu Pro Val Val Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GCTTGGAGGC	CTGGAGCGAC	GGTGTGGGTC	TGGGGGTGCA	TTGTTTCCTG	GCGAAAGTCA	60
ACTAAAGACC	ACGTTGACAC	CCTAACCGCG	GCCCGGCATG	GCCCTGTCCG	GCCTAGAGAC	120
TTTGACCGCG	GCGCAAAACG	TTGCTCTCTG	CGGCCCCATG	AGATCGCACA	CGCTTGCTTG	180
AACATCGGGT	GGAGCCGGTG	GTAACGCCAG	GCT			213

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CCGAGCTGCT	GTTCGCGCG	GGCGGTGCGG	CGCGCGCGGG	TGGGGCGGCG	ACCGAGCGCG	60
GGCCCCGGTG	TACCGCGCGG	ACCGCGCGAC	ACGCGCGAGT	CGCGCGCGAC	GGCGGATGCG	120
TGGCACCGCG	CGCGCGCGCG	GGGGCGCGCG	GGCAAGCGCG	GGCAGGTGGT	GCCCGCAGCG	180
ATGGTGGCGC	GTTCGGTGGT	ACCGCGCGGA	CGCGCGGTAC	CGCGCGCGCG	GGTGGCGCGG	240
GGGGTCCGCG	CACACTGCTG	GTGGCGCGTG	CGCGACAGGG	CGGCTTCGCG	GGCGCGCGCG	300
GACAGCGCGG	CACCGCGCGG	GGCGCGCGGA	GATGGCGTTC	TGGGGGGTGT	CAGTGGCACT	360
GGTGGTA						367

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

AAGGGGTGAT	TGGCAAGCGG	ACCGCGCGAG	GGCGCGTAGC	CGCGGGAGCG	CCGAGGCCCC	60
GACCGGACGG	GCCGGTGTCT	GACCGGGTCA	GCGACACGCG	GCGCTGACCG	TGCGCGCTCCT	120
CTACTTCGAC	GCCAGCGGCT	TGCTCAAACT	TCTCACCGAC	GAGACAGGGA	GCTCGCTTGC	180

GTCCGCTCTA	TGGACGCGCT	GCGACGCGC	ATTGTCCAC	CGCTTGGCT	ACCCGAAAGT	240
CGCGCGCGCA	CTCGCTGCAA	CGGCGCGCA	TCACGACCTA	ACCGAATCCG	AGCTCGCGCA	300
CGCCGAGCGT	GACTGGGAGG	ACTTCTGGG	CGCACCGCGC	CAGTCAACT	CACCGGACG	360
ATTGAACAGC	ACGCGCGGCA	CTCGCGCGA	ACACATGCGT	TACGCGGAGC	CGACACCGTT	420

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GTCTGTGG	TGGCATCGC	GCTACCGCGC	GAACCGCGG	CAACGCGGT	ATGCTGCGG	60
GCGCGCGCG	GCTCGCGGT	GCGCGCGGT	TCAGCTTCAG	CAGTGGCGGT	GCGCTGCGG	120
GCGCGCGCG	GCGCGGTGG	CTCTTACCA	CGGCGGTGT	GCGCGCGCG	GCTGGCGAG	180
GTACACGCG	GCGCGCGGT	GCGCGCGCG	GCGCGCGCG	GTGTTTGGT	GCGCGCGCA	240
TGGCGCGGG	GCGCGGATC	GCGGATCAG	GAACGCTCG	CACCGCGCG	GCTCGCGGG	299

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Leu	Glu	Pro	Trp	Ser	Asp	Gly	Val	Gly	Leu	Gly	Val	Asp	Ser	Phe	Ser
1					5				10					15	
Ala	Lys	Val	Asn												
			20												

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Glu	Leu	Leu	Phe	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Ala	Gly
1					5				10					15	
Thr	Asp	Gly	Gly	Pro	Gly	Ala	Thr	Gly	Gly	Thr	Gly	Gly	His	Gly	Gly


```

      20              25              30
Val Gly Gly Asp Gly Gly Trp Leu Ala Pro Gly Gly Ala Gly Gly Ala
      35              40              45
Gly Gly Gln Gly Gly Ala Gly Gly Ala Arg Ser Asp Gly Gly Ala Leu
      50              55              60
Gly Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly
      65              70              75              80
Gly Arg Gly Thr Leu Leu Leu Gly Ala Gly Gly Gln Gly Gly Leu Gly
      85              90              95
Gly Ala Gly Gly Gln Gly Gly Thr Gly Gly Gly Arg Arg Arg Trp Arg
      100              105              110
Ser Gly Gly Cys Gln Trp His Trp Trp
      115              120

```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```

Gly Val Ile Gly Lys Ala Thr Ala Gln Arg Pro Val Ala Ala Gly Arg
 1           5           10           15
Pro Arg Pro Arg Pro Gln Arg Pro Val Ser Asp Arg Val Ser Asp Gln
 20           25           30
Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

Leu Val Gly Gly Ile Gly Gly Thr Gly Gly Thr Gly Gly Asn Ala Gly
 1           5           10           15
Met Leu Ala Gly Ala Ala Gly Ala Gly Gly Ala Gly Gly Phe Ser Phe
 20           25           30
Ser Thr Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe
 35           40           45
Thr Thr Gly Gly Val Gly Gly Ala Gly Gly Gln Gly His Thr Gly Gly
 50           55           60
Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe Gly Ala Gly Gly Met
 65           70           75           80

```

Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly
 85 90 95
 Ala Gly Gly

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TCCTTTTCGG	CGCGCGCGGG	GTGGGCGGTG	TTGGCGGTGA	CGGTGTGGCA	TTCTGGGCA	60
CGGCCCCCGG	CGGCCCCCGT	CGTCCCGGCG	GCGCCGGTGG	GCTGTTCAGC	GTCCGTGGGG	120
CGGCGCGGCG	CGGCGGAATC	GGATTGCTCG	GGAACAGCGG	TGCCGGGGGG	TCGCGCGGGT	180
CGGCGCTGCT	CTGGGGCGAC	GCGCGTSCCG	GCGCGCGCGG	TGGGGTCGGG	TCCACTACCG	240
GCGGTSCCGG	CGGCGCGCGG	GGAACGCCA	GCTTGCTGGT	AA		282

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

CGGCACGAGC	CGTGCTACTG	GTCACTGAT	GCCCTGATTG	TGACCTTCCG	GCGCGCGGAT	60
CAGTGTCTCT	CAGGACCGAC	GTAATATTCG	AAAACCAATC	CGGCGCGCGA	GGCGAGGATG	120
AATGCGACAC	CGGCGCGCAT	CAGCCACGGG	AGCCACAACG	CGATGCGCGA	CGCTGCCACC	180
GAGCGCGACA	ACGCGACCAT	GATCGGCCAC	CGCTATTCGG	GACTGAAGAA	TCCAGTTCT	240
CCTGCGCGGT	CGCTGATTTC	AGCGCTTCG	TAGTCTCTGG	GCGCGGAATC	TAAACGCGCG	300
GCCACAACCC	GGAAGAAGGT	GGCGACGATC	AACGCCATGC	GCGCGGTGAG	CGCCAACGCA	360
ATGGTGGCAG	CGCACTCGAC	ACGACCGGTG	GCGAACATCG	AGGTCAACAC	GCGGT	415

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TCACCGCGTG AACGGTCTG AACACTGATA CGTATGCTTG TCAGCGAGCA GATCAAGTCC	60
AGTCCGACCA ATGCCAGGAG ATCATGGGCT AGGCTCACGG TTTCGGCTGG GACGAGACGG	120
TATTTGAGTTC TGCGGTGGGA CGGTCCGTGG CGTGGTGGGA AGTCTGACGC GGCCATCAGAA	180
CGGTGTGCAA TACCACTCTT TGGGGGATAT GGCCTATTTG GTGTCTGTGG GCGGCTCCAC	240
CGGATCCCTT TTCCAGCTTT GCGCAAGCGC GGTCCAGTTA CGGCTGTGTC ACTGCGCGCT	300
CGCGTAGCTG CGCGCGCTCG ATCGGTTTGA ACSTCATCGC AATTCGCGCA ATGGGTGAGT	360
ACCTGACGCT CCT	373

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

CCAAACCGCA CAGGCGGGCA GCGACGGTCS GAAGTTCAC CCGGTGCGG GCTCCATGTA	60
GCCAACCGGT GACCACTGGC TAGACAGCAG ATCCGTGGAT CCGCGGTTCC GTGTCTGTCG	120
GGCGGAGTAC CGCGCGGGCC AACCGCAGCC ACCAAAGCAA CCGCATCGAT ACCGGGATCG	180
CCACTCTGTC CGAATTCCAG CTCGCTGGAC AAGCTTCCGG CCGCACTCGA ACCCGGGTGA	240
ATGATTGAGT TTAACCTGCT TAGCAATAAC TAGCATACCC CTTTGGGGCC TCATAACGGG	300
TCTTGAGGGG TTTTTCCTTG AAAGGAGGAA CTATATCCCG ATAACCTGSC GTAGTAGCGA	360
AGAGGCGCGC ACCGATCGCC CTTCGCAACA GTTCCGCGAG CTGAATGGCG AATGGACGCG	420
CCC	423

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

AGTGGCCAGC CGGTGGGCA ATGCATCCAG CTCGCGGTAC GTCACTGAC GATCGGCCA	60
ACTGACGCGC ACCGAGTCAG GCTGTGCGGC AGGATTTCC GCGAACCGGG TATTCACCGC	120
GGGTGCGCAG GTCTGACAT CCGGCAGGCC GGGTCGGTC GGTCTGTGCT CGCGGTCCAG	180
CAGAATGTGC ACSTCGGCA GCGGCGGATC CCACCGGTC ACCAAGCGCT GTAACACAGC	240
CAGCAGTGGC CTGCGGAGGC TTTCCGGGCG CATCTGTCCT AGCGCACCTC GAGCACCTTC	300
CAGTACAGGC GTGAGCTGAC CGGTGCTGCG GTGCGCGGCG ACGGTCCGCG GAAAGTCCGA	360
CAAACTCTCT AGCGCCACCG GACGGAAGST CACCGGTTT CGCA	404

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

STGCTGCTCG	CAGGCTGTC	TTGGAACCG	CTGGCTAACT	TGCGACCCGG	GTATCCGGCC	60
ACCATCGAAC	CGGCCCCAAC	GGCGGTGTCA	CGGCTACTT	CGCAAGACCC	GGCGGTGTCA	120
GTGCGACCA	TAAGCGGCCA	CCCCCGGGCG	GCATATTTCG	ACAACGGCAC	CGGCCAATTG	180
GTGCTCTGCG	GGCGGGGGCG	CGATTGGGCG	GCACCGGCCA	GCATCATGGT	CTTCGATGAC	240
ATGCACGTTG	CACCGGGCGT	CATTTTTCG	CGGGGGGGCG	CAGCGCGGTT	GACCAAGCGAC	300
GACCAAGCGA	CGGCTTCTCT	TGCGGGGGCG	GGCGGCTACT	TGCTGGGGCG	CTGTCTCTCC	360
GGTCACACCG	CACGAGTGAA	TGTCGCTGAC	GCAGCGCACA	CGGATTTTAC	CGCGATCGCC	420
C						421

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATGCATATCA	CGCTCAACCG	CATCTGCGGT	GCATCTCTCG	GGGGGGGGGG	CAGTGAACTA	60
GACGAGCTGC	GGCTGCTCAT	TGCGCGGTGG	GTCACTCTGG	GCTCGCGGCT	GGCGGCGCTA	120
CGGAAAGTCA	AACGCGACTA	TGGCGCGCTT	AGCGCGGTGG	GGCGGCTGGG	CGAGTGGCGG	180
CGCCAGTAGC	ACACTGTTCAT	CGACGAGCTC	ATCGAAGCGG	AGCGGGGCGA	CGCGAACTTC	240
GGCGATCGGA	CGGACGTTTT	GGCGTTGATG	CTCGCGCAGCA	CTTACGACGA	CGGTTCCATC	300
ATGTGCGGCA	AGGACATTGG	CGACGAACTG	CTCACGCTGC	TTGCGGGGGG	GCACGAAACC	360
ACGCGGGGCA	CATGGGCTGG	GGTTGCGAAC	GGCTCAACCG	GCACCCCGAC	GTGCTCGCGG	420
CTCTGG						426

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GTCTTGCTCG	CAGGCTGTC	TTGGAACCG	CTGGCTAACT	TGCGACCCGG	GTATCCGGCC	60
ACCATCGAAC	CGGCCCCAAC	GGCGGTGTCA	CGGCTACTT	CGCAAGACCC	GGCGGTGTCA	120
GTGCGACCA	TAAGCGGCCA	CCCCCGGGCG	GCATATTTCG	ACAACGGCAC	CGGCCAATTG	180
GTGCTCTGCG	GGCGGGGGCG	CGATTGGGCG	GCACCGGCCA	GCATCATGGT	CTTCGATGAC	240
ATGCACGTTG	CACCGGGCGT	CATTTTTCG	CGGGGGGGCG	CAGCGCGGTT	GACCAAGCGAC	300
GACCAAGCGA	CGGCTTCTCT	TGCGGGGGCG	GGCGGCTACT	TGCTGGGGCG	CTGTCTCTCC	360
GGTCACACCG	CACGAGTGAA	TGTCGCTGAC	GCAGCGCACA	CGGATTTTAC	CGCGATCGCC	420

CGCCGCTCCG ACCGCAAGCT GGTGCTGGGC AGCCGAGATG GCGCCCTCTA CACGCTTGCC
AAGAACCOCG ASTTGACCGG CGTCGGCGCC GCCACCTAG CC

480
522

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GTGCGGCGCC	ACGCGCTCC	GGCGGCCCCA	GCCTCTGGGC	CCAGACCCCG	CGCAAAACCA	60
ACCCGTGGCC	CTTAGTGGCC	GGCGGCGGCG	CGCTCTGGCT	CGTCTCTG	TTGGGCGCCA	120
TGCGCTCTG	GATCGGCATC	CGGCGCAAGC	CGGTACAGCC	CGCTCAGCCG	CTTGGCGAGG	180
AGCGCGTTAG	CGCTCTACTG	CTGACTCTCT	CAGAACTCAA	CGCGGTGATG	GGCTCTCTCT	240
CCATCGAGCC	GGGCAAAACG	ATGACATCGA	TGGACTCTTC	CGCGGTGACG	GTGCTCTCTG	300
CGGACTGCCA	GGGCGGCTG	TATACCAAGC	AGGATCGGCT	GTATGCCGCG	ACCGGCTACA	360
CGGCTATCAA	CGGCTTGATT	TCATCCGAGC	CGGCGGACAA	CTACGAACAT	TGGTGCAACC	420
AAGCGCTCGT	CGCTTTTGGG	ACCGGCTACA	AAGCGGCGCG	GTCTGTGCAG	ACTTGGGCGG	480
ACAAATGGAA	GACTGGGCGA	GGCAAGACGG	TCACCTGCAC	GAATAAGGCT	AAGACCTAAC	540
GGTGGACGTT	TGCGGACGTC	AAAGCGAGCC	CGCCGACGAT	CACGCTGATA	GACACCCCAAG	600
AAGCGGCTGA	GGCTGTGGGA	TGCCACCGCG	CGATGAGCGT	GGCCCAACAT	GTGTTTGTGG	660
ACGTCAACGC	ATGCGGGTAC	CAGATCACCA	ATCAAGCAGG	CCAGATCGCC	GCCAGATCTT	720
GTTCACAAG	TCACAAGG					739

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

AGAGCTCTCT	GAGGCGGCGA	TGCGGCGCGG	CGAAGCGGTT	AACCGCGGAC	TGAACCGGTT	60
GGCTATGC						69

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

ACTGCACCCG	GCAGGCGCGA	CCNACGGATC	GGGTCAACTA	GCACCTGCCG	TGGAGGCGCC	60
CCCGCGGTCT	GTGCCTTCCC	ACGCGGAACC	CTTGGGCGAG	CGGGCTCCAG	AAGGGTTGGA	120
GGGAGAGTTG	GAGGACCGTA	TCGACGAGCG	GTTCGCGGTC	TTGAGCTCGG	CCAGTCTCGC	180
CGAAGCGCTG	CCGGGTCCGC	TGACCCGAT	GAGCGTGGAT	GTCCAGTTGA	GTGACTCGG	240
CCCGCCCGGT	CGGGCGATGG	GTCCGGTACT	GGCGCTTGGC	GGTGTGCTTG	CCGATGAGTG	300
GGAGAGAAGA	GCCATCCGCG	TGTTGGGTCA	CCGCCCGTAT	ATCGAGTGT	CGGCCAATAT	360
TGTGCGCGCC	GCCCAACTGC	CGGGGTGGGA	CGCGCAGGCC	GTACCCCGGC	GGGCACTGG	420
CGAGCAACCG	CAGGTCACTG	AGCTGCTCC	GTTTGGTGA	CGCAACTTG	CGGGCGGACC	480
GCTCGGCTCG	GTGCGGAAGG	TGTCGTGAC	GGCACGGTGS	CTG		523

(2) INFORMATION FOR SEQ ID NO:272:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GTGTGGGTGT	CGTCGGGCTA	GGAGCGACTT	CCCGCGCGCG	CGCGCGCGCC	GGAGCGGGGT	60
GTGACGGAAC	CGGTGCCCGG	CCCGCGCGCG	GGCGGACCAA	AGCGCGGATC	GATTTCGGCA	120
GGCGCTTGGC	CGCGCTTGGC	TCCACCGGCT	TGTTGGCGGT	CCGAGCGCAT	ACCACAAACC	180
AACGCTGAAG	GGCGCGCGCG	TCCGTTGGCT	TGCGCGCGCG	CGAC		224

(2) INFORMATION FOR SEQ ID NO:273:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TGAAGTGAAT	CGCGCGCTCG	ATCGCGCGCG	CGCGCGCTGC	ATAGCTGCGC	CGCCAGGCCA	60
TGAAGTGCCT	TTCGCGCATG	CGCGCGCTCG	TCTCGCGCTT	GTCCCAACCC	TGCAGCGCGC	120
CGAGTGGGCG	TTCGCTGAGC	CGCCAGCTAC	CGCGCGCGCG	AATCCAGAGC	CGATCGGCGC	180
TGTCCAAACG	CAGATGCGCG	GTGGTGATCG	CGCGCGCGCG	CAACGAGGTG	TAGAGCAAGT	240
CGGGCAATAG	GTCTGTTTCC	CGCATCACTC	CGCGCGCTCG	AACCGCTTCT	CGCTGGCGCT	300
TGTCCGTCAG	CGCGACATCG	ACCCAGCGCG	TGAACAGGTT	GAGGCGATTC	CAGTGCCTCT	360
CGCGGTGGCG	CAGCAACACC	AGGCTGCCAG	TGTTTGGCAT	ACCGCAAGT	CTCTCAGCGA	420
CTCCCGCACT	CTTCATCGTG	GACCAAAATG	CGCGAATCTC	CGTCGCTCG	CTGCGCGCGC	480
CGTTCATACC	CGCGAGGTGS	TGCGCACTCT	AACGCGCGGT	T		521

(2) INFORMATION FOR SEQ ID NO:274:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(11) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTCCAGGCTC	ATTCTGTGTA	ACAAAGCCAC	CCGCGCGTAC	AGCGGACGCC	CCCATTCTGT	60
GTCTGTATAG	TCCGCGTACA	GCTGGGCTAT	GGGCGCTTGA	CGAAGCTTCG	CCGAGGGGCA	120
GGGAACGAGC	CCGTCGCGCC	TCACGCGGGG	TCAGAACGGT	AGTGCACGAC	AGTCTCGCCG	180
CGGGAAGGTT	TTGACGCGTC	AGACTCGGCC	TGGCGCTCTT	CGGACGAGGC	GTGGATCGCC	240
CCGAGCTGAG	AGCGTAGCGC	CTGGAGCTCA	CGGCCGAGCC	GTTCACGACG	CCAGTCCACC	300
TGCTGTGCTT	TGTTCCCGCG	CAGCAGCTGC	GTGAACCTTG	CCGCGTCGAC	ATCGGCGGCG	360
GTGACCCCGA	ACGCCGCGAG	CTGCTCGGCC	GTGCTCGGCC	CGCGCAGGGG	CGGCAACTGC	420
TGCGCA						426

(12) INFORMATION FOR SEQ ID NO:275:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(11) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GGCGACACGG	CGGACAAGC	GCAATCGGCC	TGGCGCGCGG	CGCGCGCGCG	GACCGGGGGC	60
AGGCGCGCGC	CGGCGCGCGA	CTGTGGGCTA	CTGCGCGCGC	CGCGCGACAC	GGCGGGGCAA	120
GGCGGTGCTA	CGGCGGGGCT	ACCGCTGCCC	GGTCAGGCAG	GCATCGCGCG	CGCGGGTGGC	180
GGCGGTGGGC	TGATCTGCAA	CGGCGGGGCT	GGCGGGAC			219

(12) INFORMATION FOR SEQ ID NO:276:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(11) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AAGATCATCG	GCGCGCGTCC	TTAGCATCGC	TGGCTCTGCG	ATCGTGGCCG	GGCGGATCA	60
CGGAGGTTCG	GCTTGTATCC	CGACTCTCTG	AACGGTCAGC	ACCACAGTGG	GGTTCCTGGG	120
ATCTCTTTCC	ACCTTGGGCC	GCAGACGGTG	GACATGCACT	TTGACCAAGC	TGGTATCGCG	180
TGGGTGCGCG	TAAACCCATA	CGTGTTCGAG	CAGCACATCA	CGAGTAAACA	CCTGGCGCGG	240
CTTGCAGGCC	AATGCGACCA	ACAGGTCGAA	TTCCAGCGGT	GTCAACGAGA	CTGTCTCACC	300
GTTCGAGAGT	ACCTTGTGCG	CGGTACGCTC	GATTCTCTAG	TGGCGGATGG	ACAGCATCTC	360
GGCGGGTTCC	TGCTGTCTGC	GGCGGAGCGG	CGGCGGACCC	CGCGCAACCA	GCTCTTTGGG	420
CTTGAACGCG	TTGATGATGT	AGTCGTGCGC	CGCGGACTCC	AGACCTGACA	CCACATCCAC	480
GCTGTCTGTC	TTTTCGCTGA	GCATCAAGAT	CGGAACACCG	GAATCGCGCG	GCAACACCGG	540
GCACAGCTCG	ATGCGCTTCA	TACTGGGGCA	A			571

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Leu Phe Gly Ala Gly Gly Val Gly Gly Val Gly Gly Asp Gly Val Ala
 1             5             10             15
Phe Leu Gly Thr Ala Pro Gly Gly Pro Gly Gly Ala Gly Gly Ala Gly
 20             25             30
Gly Leu Phe Ser Val Gly Gly Ala Gly Gly Ala Gly Gly Ile Gly Leu
 35             40             45
Val Gly Asn Ser Gly Ala Gly Gly Ser Gly Gly Ser Ala Leu Leu Trp
 50             55             60
Gly Asp Gly Gly Ala Gly Gly Ala Gly Gly Val Gly Ser Thr Thr Gly
 65             70             75             80
Gly Ala Gly Gly Ala Gly Gly Asn Ala Ser Leu Leu Val
          85             90

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Pro Pro Val Ser Ala Asn Ala Met Val Pro Ala His Ser Thr Pro
 1             5             10             15
Pro Val Ala Asn Ile Glu Val Asn Thr Pro
 20             25

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Lys Pro Asp Arg Pro Ala Ala Thr Val Gly Ser Cys Thr Thr Val Arg
 1 5 10 15
 Ala Pro Cys Ser Gln Pro Val Thr Thr Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:280:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Trp Pro Ala Gly Arg Pro Met His Pro Ala Pro Gly Thr Ser Ala Asp
 1 5 10 15
 His Pro Pro Asn
 20

(2) INFORMATION FOR SEQ ID NO:281:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1 5 10 15
 Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
 20 25 30
 Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
 35 40 45
 Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
 50 55 60
 Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
 65 70 75 80
 Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
 85 90 95
 Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
 100 105 110
 Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala
 130 135 140

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly
 1           5           10           15
Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr
 20           25           30
Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly
 35           40           45
Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Gln Tyr Asp
 50           55           60
Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn Phe
 65           70           75           80
Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp
 85           90           95
Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr
100          105          110
Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg
115          120          125
Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp
130          135          140

```

(i) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1           5           10           15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Glu Pro Ala Val Ser Pro Pro
 20           25           30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
 35           40           45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
 50           55           60
Pro Gly Ala Asp Ser Ala Ala Pro*Ala Ser Ile Met Val Phe Asp Asp
 65           70           75           80
Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
 85           90           95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
100          105          110

```

237

Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp
 130 135 140
 Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Ieu Ala
 145 150 155 160
 Lys Asn Pro

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro
 1 5 10 15
 Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Val Val
 20 25 30
 Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro
 35 40 45
 Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala
 50 55 60
 Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser
 65 70 75 80
 Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr
 85 90 95
 Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro
 100 105 110
 Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser
 115 120 125
 Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala
 130 135 140
 Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp
 145 150 155 160
 Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala
 165 170 175
 Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr
 180 185 190
 Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln
 195 200 205
 Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys
 210 215 220
 Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:

238

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
 1             5             10             15
Leu Asn Ala Leu Ala Tyr
                20

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
 1             5             10             15
Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
 20             25             30
Ser Ala Ala Pro Glu Gly Leu Glu Gly Glu Phe Asp Asp Arg Ile Asp
 35             40             45
Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
 50             55             60
Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
 65             70             75             80
Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
 85             90             95
Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
100            105            110
Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Glu Leu Pro Gly
115            120            125
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln
130            135            140
Val Thr Glu Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro
145            150            155            160
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu
165            170

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

Val Gly Val Val Gly Val Gly Ala Thr Ser Pro Ala Gly Ala Gly Ala
 1             5             10             15
Gly Ala Gly Ser Ala Gly Thr Gly Ala Gly Ala Gly Gly Gly Ala Thr
 20
Lys Gly Arg Ile Asp Ser Ala Ser Ala Leu Ala Ala Pro Leu Ser Thr
 35             40             45
Gly Leu Leu Ala Val Pro Ser His Thr Thr Asn Gln Arg
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

Met Ala Asn Thr Gly Ser Leu Val Leu Leu Arg His Gly Glu Ser Asp
 1             5             10             15
Trp Asn Ala Leu Asn Leu Phe Thr Gly Trp Val Asp Val Gly Leu Thr
 20
Asp Lys Gly Gln Ala Glu Ala Val Arg Ser Gly Glu Leu Ile Ala Glu
 35             40             45
His Asp Leu Leu Pro Asp Val Leu Tyr Thr Ser Leu Leu Arg Arg Ala
 50             55             60
Ile Thr Thr Ala His Leu Ala Leu Asp Ser Ala Asp Arg Leu Trp Ile
 65             70             75
Pro Val Arg Arg Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu
 80             85             90
Gln Gly Leu Asp Lys Ala Gln Thr Lys Ala Arg Tyr Gly Glu Glu Gln
 100             105             110
Phe Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Ile Gln
 115             120             125
Arg Gly Ser Gln Phe
 130

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Pro Gly Ser Phe Ala Arg Thr Lys Pro Pro Gly Arg Thr Ala Asp Ala
 1             5             10             15
Pro Ile Arg Cys Arg Asp Ser Arg Gly Thr Ala Gly His Arg Ala Leu
 20             25             30
Asp Glu Pro Pro Pro Arg Gly Ser Glu Pro Ala Arg Arg Ser Arg
 35             40             45
Gly Val Arg Thr Val Val His Asp Ser Leu Ala Ala Arg Arg Val
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly Gly
 1             5             10             15
Asp Gly Gly Gln Gly Gly Ala Gly Arg Gly Leu Trp Gly Thr Gly Gly
 20             25             30
Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala
 35             40             45
Ala Arg Ser Gly Arg His Gly Arg Arg Gly Trp Arg Arg Trp Ala Asp
 50             55             60
Arg Gln Arg Arg Gly Arg Arg Arg
 65             70

```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```

Asp His Arg Arg Ser Leu Ala Ser Leu Arg Ser Ala Ser Ser Pro
 1             5             10             15
Ala Arg Ile Thr Glu Val Arg Pro Cys Thr Pro Leu Leu Glu Arg Ser
 20             25             30
Ala Pro Gln Ser Gly Ser Arg Asp Pro Phe Arg Pro Trp Pro Ala Asp
 35             40             45
Ala Gly His Ala Arg Ser Pro Ala Trp Tyr Arg Leu Gly Ala Gly Asn
 50             55             60

```

Pro Ile Pro Val Arg Ala Ala His His Glu
65 70

(2) INFORMATION FOR SEQ ID NO:292:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(21) MOLECULE TYPE: COND

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

CGGCGAGTAA	CACCGTGAAT	TGAAGGAGAC	CGCTGGTCTT	GGGCGGATTC	TATCGTGGG	60
GGAGCGGTTA	TTGACGGGCC	CGAGGCGCACT	CGCGTGCAC	CAAGTGGTGA	CTCAGCGCGT	120
TTTCAGGACA	ACGAAAGGCG	GACACACAC	TTGACATTCG	ACAGCAGGCG	CGCG	180

(2) INFORMATION FOR SEQ ID NO:293:

(1) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 404 base pair
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 293.

TCGACCAAGC	GGTGACATC	GCTCCGGTGG	CGCTAGAGAG	TTTGTCCGAC	TTTCCGGTGA	60
TCGTGTCGCG	GACCTCAGCG	ACGGGTGAGC	TCACGCTCTC	AGTGGAGGCT	CTCAGCGGTG	120
TCGTGCGGAC	GATGGCGCGC	GAAGAGTGGT	CGACGCGGGT	CTCGGCTGTG	TTACAGCGCT	180
TCGTTCAGCG	TGTGGATTCGG	CTGGTGGCGC	CGACTGCACAT	TCCTGCTGAC	GGGACGACGG	240
TCGACCAAGC	ACCCGCGGCT	CGGATATGTA	ACAGCTTCGAC	ACCGCGCGGT	CATACCGGCT	300
TCGCGCAAAAT	CGCTCGCGCA	CGCTGCTGAC	TCGTTGGCGT	CAATTGGGCG	GATGGCTCAGC	360
TGACGTACCG	GGAGCTGGAT	GCAATGGCGT	ACCGGCTGGC	CACCT		420

(2) INFORMATION FOR SEQ ID NO:294:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ala Asn Gly Val Thr Phe Arg Pro Val Ala Leu Glu Ser Leu Ser His
1 5 10 15
Phe Pro Val Thr Val Ala Ala His Arg Ser Thr Gly Glu Leu Thr Leu
20 25 30

242

Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser
 35 40 45
 Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp
 50 55 60
 Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp
 65 70 75 80
 Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val
 85 90 95
 His Thr Arg Phe Ala Glu Ile Ala Ala Ala Gln Pro Asp Ser Val Ala
 100 105 110
 Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu
 115 120 125
 Ala Asp Arg Leu Ala Thr
 130

(2) INFORMATION FOR SEQ ID NO:295:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(12) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GCTTCGACCG	CTACGAGTAC	CTGTTCTGGG	TGGGTTGTGC	GGGCGCTTAC	GACGACAGAG	60
GCAGAGAGAC	CACCAAGGCC	GTCCGCCGAGC	TGTTCCGCGT	CGCCGGGGTG	AAATACTTGG	120
TGCTGGGGCG	TGGGGAACCC	TGCACGCGCG	ACTCGGCGCG	CGCTCCGGGC	AACGAGTTCC	180
TCTTCGACCA	GCTGGCACAA	CAGGCGCTCG	AGACCGTGGG	CGGTTTGTTC	GAGGTTGTGG	240
AGACGCTGGA	CGCGAAGATC	GTGTCACCTT	GCCGCGACTG	CTTCACACCG	ATCGGCACGG	300
AATATCGGCA	GCTGGGCGCC	AATACACCGG	TGCTGCAACG	CACTCCAGCTG	CTCAATCGGT	360
TGGTGCACGA	CAAGAGCGTG	GTCCGTGTCA	CTCCGGTTTC	TCAAGGACATC	ACCTACCAAG	420
ACCGCTGCTA	CTGCGGCTCG	CACACACAGG	TGTACGAGCG	ACACCGGAGG	CTGATCGGTT	480
CCGCGGGGCG	CACCTGAGCC	GAGATGCCCG	GCCATGCCGA	CCGCGAG		526

(2) INFORMATION FOR SEQ ID NO:296:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(12) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CTCCGCGCGG	TGATCTGGCC	GGCGAAGTTC	GTCACTGCAT	CCAGACCCCA	ACGATCTGCG	60
ATCAGGCGCG	TGCGCATGAT	CACCGCAGCG	GCCACACGCA	CCCGGGGCGT	GCCGCTGGAA	120
TAGACGAAAC	CCCGGTTGAG	TGCGGGAAGC	TGGGAGGCAA	GAAAGACGCG	GCCGACCAATG	180
CCGAGGAACA	TGCGCACTCC	ACCGATCCGA	GGGCTAGCGC	TGACCTGCAC	ATCTCGCTCC	240
CCCGGCTAGG	CGACGCTTCC	CAGGCGACTG	GCCAGCATCC	GCACCGGACC	GCTCGCAAAA	300
TAGGTGATGA	TGCGCGCGGT	CAGCGCGAGC	AGCGCAGACT	CACCGACCGG	GACACCGGCG	360

CCGCGATAGG ACAGGGCGAG CAAGCCACCG GCAAGCGCGG CCACATCGCT GGACACCTCG 420
 AGACCGTACT GCACCAACTG GAAGAGCTGA AACTCGCGCG AACGTGCAAC AGCTCGAAC 480
 AATTGGG 487

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

ACGAAGCGCG AGAATATGAG CCGGGGCAAC CGGCGATGTA CGAGCTTGAG TTCGGCGCGC 60
 CTCAGCTGTC GTGCTCGGAC GCGCTTGCTC CGGTGTGGGT GCACGCTTTG GAAGGTTTCT 120
 CGCAGCGCGG GCATGCGGATC CGCTGCGCGG CGCGCCACTT CAAGCGCGGC CTGGACACAG 180
 AGCTGCTGCG GTGCTTGGCG ATCGATGAAC TACTGGACTA CGCTCGCGCG CGGCCATTAA 240
 TGACTTTCAA GACCGATCAT TTCACCCACT CGGATGATCC TGAGCTAAGC CTGTATGCGC 300
 TCGCGGACAG CATCGGCACC CCACTTCTGC TCGTGGCGCG TTGGGAGCGG GACCTGAAGT 360
 GGGAGCGGTT CATGACCGCC GTCCGATTGC TGGCGGAGCG CCGCGGTTGA CGGAGAACCT 420
 ATGCGCTTGG GCACCGTCTC GATGCGCTT CGGCACACAC GACCGATCAC GATGACCGCT 480
 GATTTCACAA ACCGCGAGCT ATCTCGGATT TTCACCGGTT CGATCTCC 528

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

CCAGCGCTGT CAAGGAGCGG GTGCGCGGCT TGCCTCGGTT GCGCGCGAGG CGGCGGTTGC 60
 CGCGCTTGCC GCGGTTGCGG CGGTACCGG GGTTCCTTAC GGTGCGCGCG CGCGCGAGCA 120
 TGGCGCGGCT GTTAGGCGG TTTCGCGCGG CCGCGCCCTC ACCGCGCTTG CGGCATGCG 180
 GCGCTTGCC GCGGCTGGTG GCGGTGGCGG CTGTGTTGAC CTGCTGAGG GTATTGTTCC ACCGCGCGCG 240
 CGCTTGACC TTGCGCGGTG TCGATGCGCG CTGTGATGGA TCGCGCGGAC ACAGAGTTGG 300
 AAGCTTGCCG TCGCGCGCGA GCGGCCAAC TGTGTGCGCG CTCTGCGAT TTGCGCGCGG 360
 CGACAGATG GATGCGCACC ACCGAGCGCT GCGGCCCTCT GGGGAGGCG AGCGCGGCTT 420
 CGCGCTCAC CCATACGCGA CGGTGCGCGG CGGCTTCGGA GATTTCAGG CTGCGTTGCA 480
 CCAGATCGAG CAGCGGTGTT CCGAGGACT GGGTTAGCGG GTTGGCGCGG CCGTTGTAGC 540
 GCGAGCGCA ATATCGGTGC CCACTCGACC CAACCGGAGC TCCATAAGCG ACACCATGCG 600
 CGGTTGATGC 610

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid

244

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

Phe Asp Gly Tyr Glu Tyr Leu Phe Trp Val Gly Cys Ala Gly Ala Tyr
 1      5      10      15
Asp Asp Lys Ala Lys Lys Thr Thr Lys Ala Val Ala Glu Leu Phe Ala
 20      25      30
Val Ala Gly Val Lys Tyr Leu Val Leu Gly Ala Gly Glu Thr Cys Asn
 35      40      45
Gly Asp Ser Ala Arg Arg Ser Gly Asn Glu Phe Leu Phe Gln Gln Leu
 50      55      60
Ala Gln Gln Ala Val Glu Thr Leu Asp Gly Leu Phe Glu Gly Val Gln
 65      70      75      80
Thr Val Asp Arg Lys Ile Val Val Thr Cys Pro His Cys Phe Asn Thr
 85      90      95
Ile Gly Lys Glu Tyr Arg Gln Leu Gly Ala Asn Tyr Thr Val Leu His
100     105     110
His Thr Gln Leu Leu Asn Arg Leu Val Arg Asp Lys Arg Leu Val Pro
115     120     125
Val Thr Pro Val Ser Gln Asp Ile Thr Tyr His Asp Pro Cys Tyr Leu
130     135     140
Gly Arg His Asn Lys Val Tyr Glu Ala Pro Arg Glu Leu Ile Gly Ala
145     150     155     160
Ala Gly Ala Thr

```

(12) INFORMATION FOR SEQ ID NO:300:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro
 1      5      10      15
Thr Ile Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln
 20      25      30
His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg
 35      40      45
Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Glu His Arg
 50      55      60
Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro
 65      70      75      80
Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr
 85      90      95
Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys

```

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```

      100      105      110
Leu Thr Gln Arg Asp Thr Gly Ala Ala Ile Gly Gln Gly Gln Gln Ala
      115      120      125
Thr Gly Asn Ala Gly His Ile Ala Gly His Leu Glu Thr Val Leu His
      130      135      140
Gln Pro Glu Glu Leu Asn Thr Arg Arg Thr Cys Asn Ser Cys Glu Gln
      145      150      155      160
Leu

```

(2) INFORMATION FOR SEQ ID NO:301:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

Glu Ala Arg Gln Tyr Glu Pro Gly Gln Pro Gly Met Tyr Gln Leu Glu
 1      5      10      15
Phe Pro Ala Pro Gln Leu Ser Ser Ser Asp Gly Arg Gly Pro Val Leu
      20      25      30
Val His Ala Leu Glu Gly Phe Ser Asp Ala Gly His Ala Ile Arg Leu
      35      40      45
Ala Ala Ala His Leu Lys Ala Ala Leu Asp Thr Glu Leu Val Ala Ser
      50      55      60
Phe Ala Ile Asp Glu Leu Leu Asp Tyr Arg Ser Arg Arg Pro Leu Met
      65      70      75      80
Thr Phe Lys Thr Asp His Phe Thr His Ser Asp Asp Pro Glu Leu Ser
      85      90      95
Leu Tyr Ala Leu Arg Asp Ser Ile Gly Thr Pro Phe Leu Leu Ala
      100      105      110
Gly Leu Glu Pro Asp Leu Lys Trp Glu Arg Phe Ile Thr Ala Val Arg
      115      120      125
Leu Leu Ala Glu Arg Leu Gly Val Arg Gln Asn His Arg Pro Gly His
      130      135      140
Arg Pro Asp Gly Arg Ser Ala His Thr Thr Asp His Asp Asp Arg Ser
      145      150      155      160
Phe Gln Gln Pro Gly Ala Ile Ser Asp Phe Gln Pro Phe Asp Leu
      165      170      175

```

(2) INFORMATION FOR SEQ ID NO:302:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Lys Pro Val Lys Glu Pro Val Pro Ala Leu Pro Pro Val Pro Pro Thr
 1      5      10      15
Pro Ala Leu Pro Pro Leu Pro Pro Leu Pro Pro Val Pro Gly Phe Pro
 20      25      30
Thr Val Pro Pro Gly Ser Met Ala Pro Leu Phe Arg Pro Phe Ser
 35      40      45
Pro Ala Pro Pro Ser Pro Ala Leu Pro Pro Ser Pro Pro Leu Pro Pro
 50      55      60
Leu Val Gly Val Ala Trp Leu Thr Tyr Cys Ser Thr Gly Pro Ala
 65      70      75      80
Leu Asp Pro Leu Ala Val Ser Ile Ala Ala Ser Met Asp Pro Pro Thr
 85      90      95
Thr Thr Cys Glu Ala Ser Pro Ala Ala Ala Ala Glu Leu Cys Arg
 100     105     110
Gly Ser Cys Asp Leu Ala Pro Ala Asp Glu Met Met Gly Thr Thr Gly
 115     120     125
Ala Cys Gly Arg Leu Gly Glu Ala Ser Ala Gly Ser Arg Ser Arg His
 130     135     140
Thr Arg Arg Cys Ala Ala Ser Glu Ile Cys Arg Leu Arg Cys Thr
 145     150     155     160
Arg Ser Ser Ser Gly Val Pro Arg Asp Trp Val Ser Pro Leu Ala Pro
 165     170     175
Pro Leu

```

(12) INFORMATION FOR SEQ ID NO:303:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

AATTCGGGAC GARCAGCAGT AACACCGGCT TCTTCAACTC CGGCGACGTC AATACCGGTA      60
TGGGCAACAC CGGCGAGTTC AACACCGGCA GCTTCAATCC GGGCGATTCC AACACCGGGG      120
ATTTCACACC ANKACAGCTAC CACACGGGGA CTCGGAACAC CGGGCGATTTC TACACCGGCG      180
CCTTCATCTC CGGCGAGCTAC AGCAACGGGT CTGTGGAGT GGAATATTAT AGGGCTCATT      240
GGNTGACACC GGGCTTTCGA ATCCCTCGXG CCAATTCAAC TCTTCNACAA GCTTGGGGCC      300
GCATCTBACG CGGGCTGAAT GATTGAGTTT AACCGCTNAN CAATRACTAG CATACCCCTT      360
TGGGCGCTCT AAACGGGTCT TGAAGGGTTT TTTGCTGAAG GGANGAATA TATCCGATA      420
ACTGCGGTAN TACGAAAGC CGCACCGATC GCCTTCCCAA CAGTTGCGCA CCKGAATGGC      480
AATGACCCNC CCKTTACCG GGCATTAAAC CGGGGCTGTN GSKTTTACCC CCACGTTACC      540
GCTACCTTGC CANNSSGCTN RSGCGGTCTT TCTTTCTTC CTTCCTTCTC CCMCTTCGGC      600
GGTTCCTTTC AGCTCTAAAT CGGGGNNCCC TTTMGGGTTC CAATTATTGC TTACNNSCCC      660
CCACCCCAAA AAYTNATTNG GGTTAATGTC CCTTMTGGG CNCCCCCTA WTNANNTTTC      720
TCCCCCTTNA CTTTGRSTCC CTTCTTTATN NTGAGNCTNT TTCCACYGGA AAAMNCTCCA      780
CNTTYSGGG TTTCTTTTGA WTTATPRGGR AATTSCAATY CCGCYTTGGG TTAANNTTAA      840
CCTATTTCNA ATTTTCCCGM TTTTGNATR TTNNCKCGM KNTCCGNKA SGGTTTTCCT      900
CCCCCTTSSG GKTCTCCCGN G

```

(2) INFORMATION FOR SEQ ID NO:304:

(A) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:304:

AATTGGGAC	GAGATANGGG	NGCAGCGGGG	TCCGCGAGCG	CGCGGACCGT	CGCCAGCACC	60
ACGGGGGTCA	ACAGCACCAC	GCTGGCTTCC	ANGCAGAGCG	CGCGGCTGAT	GGCGGCGGAG	120
ACGGGCAACA	CCTGGCGTAG	CAGTGGGTGC	GACTCGCGCG	TGGCTCGANC	CATGGCGGCG	180
CGGGGTGGCT	CGAACGAGCC	TTGGTGGTCC	ACAGGTTAGC	CAGCAGCCAA	ACCGCACCCA	240
GAAACCCACA	CGCGGCGCGC	CGCGGAGACT	TGGCGCATCG	CTGTGTGGGG	CGAATTTGCC	300
CGATCGCTNA	CAGGATGACC	CCTGCCGGAA	CGCGGCGGCT	CGCTCGGGGG	AGCGCGGTGG	360
CGCGGCGCAC	CGCGAACCCA	NGAACACGGC	AAGCAGTATC	ANGCGAACAG	CAATTGTCAA	420
GGGTAAAGCG	CTTCACATCC	AGGGATCTCG	CGGGGCCACA	CGGTGCGGTC	TGCAGSGGCA	480
CGCGTCTCTN	GGGCGGNCAC	TCTTCAAGAA	TGCGATCTNA	CAGGCTAGGT	CTTGGCGGCA	540
TATGSAAGGN	CGCACCGGCT	TTAAAGCGGC	SAAAAAATC	TCCGANTGGA	TAAATTCAGC	600
CGCGGAGGCC	CGGTGSGGNN	NGTCGCGGKC	ATTTTCAAC	MGGTTTACG	CGCGGTTCGG	660
GCGAAGTCAG	CAAAATTAGG	CTNGGGGNTY	CGGGCGGCTA	ACCGCGNTK	NGCGCTTAA	720
AAAAACCGGC	TTTTCTGATC	TAMMACCGGN	CGCCGANTGG	CGGKTGKTCC	CAGGNTTAA	780
AMCTGCTGSS	MNGGGGTGGG	SAACCGTTCC	CGNGGGGTTT	NTGCTTTCYT	AMGCGCGCGG	840
AAACGCGKYG	GGGTGGKRTN	MASSAMNCCG	CMGTYTCTT	TAAAGGCCAN	ENRAANGKYT	900
CCTTGGGAAG	CTTNCATATC	GAAATATCTC	CTTNGGSSCN	CTTTCNRTYN	NRNGGGLAGC	960
AMTITTCGNC	GTTTCANTCG	GGTCCGASHN	AAACGCTTCT	CTTTCGSSCC	STCCGGSNTK	1020
GGTGTANANAN	AAASATTTTC	TYCBBNANKE	TYTGGGCTTT	CYTMGRRNR	CMGAACCTCG	1080
GS						1082

(2) INFORMATION FOR SEQ ID NO:305:

(A) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:305:

AATTGGGAC	AGTGTATCGG	CTGAAGCGGG	TAGCGCGGGT	GGCTCGGGTT	GTTTGCGAAC	60
RAAATCGGCT	CGAAGTGGGT	TGGGTAGGCG	GTGTCCANAA	CGGTGCGGCG	GTGCGGCGCG	120
ATCTGATCGG	CGCGGCGGTA	GTGACAGTGC	CGGGGCGTGT	CGAGTCCGAT	CGCGGAGATG	180
TTGTGTTGCT	GTTGTATCCA	CGCGAAGAAC	CGGTGCGAGT	CGACCGCGGC	CGCTTCGATC	240
GACTCGAAGC	GTTCGCGGAA	ATCGGGCGCG	TACTTGAAGG	TCTTGAACCT	GCGCTCGAGC	300
AACGGGTGCT	CTTCTGTGTT	TGCGGGCGGT	AGTGGCACTT	GGTGCACCG	AACTCGGGCA	360
NCAMKARNC	CACCGGTTTG	GAACTCATCC	ACAACCCCGG	TGCGGCTCNA	GCTCACTTGT	420
NGCGGCTDAA	TTTTTGTGGG	GGCAAGGGTT	TGCGGAYCAN	KCGGCTCGGC	CAAAACTTCC	480
ANTGNCSCGA	AGGCGNCCTT	CNGCCCAAC	AMGTTACGGG	ANAAANATY	CAAGAGYACG	540
CYTGGGKTN	TTACANTCTC	CGTTTGGSTY	GGGCCCCGNN	CYTTGKNAT	AGGCTCTNCA	600

ANTCCCAACN	CCKCCCAANA	RCYKGGGGGCC	CCNCCCAACC	CGGGKGAAGA	WTAATTTAAA	660
CCCAACAAW	ACTMMHACC	CNNGGGGGCCY	AAACGTTTNR	AGGTTTTSCT	NAAAGAAASA	720
ANTCGGAAC	CGGNTSTACC	AAAAASCCCK	CCNNTCCCTC	CRASATTGSC	NCCSAAWKSA	780
AKSCCCCNFY	TCCSCNNHC	CSGCGGKKKT	KEGTNCCCT	MMRCNMWYTS	GGCCNASCCN	840
CKYSSMYCC	CCCTTCCCM	CTCCGKTKCC	CCAMCCYANC	MGGCCCCYTM	GEKCCCKWKT	900
YKCCCCCCC	ATGNNNGGG	NGACCTTNGG	CCCCMKRRGM	TCCCNANTGA	MCCTCNGNRA	960
MXCYCCNRAR	ANMCCSCNCC	NGCNCRCNN				990

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

AATTGGGTG	CCAACCGGG	CTTGTTCGG	AACGGCGGG	CCGTTGGTGC	CGGTGGGGCT	60
GGTGGTGGC	CGGCGCGGC	GGCGGTAAC	GCGGGTGGT	TGGTTCATG	GGGCGCTGGC	120
GGCGTGGGT	GTGTAKTGC	GGCGGGGGC	AACGGTCTA	CCCGCGGTCA	GGATGGGGCG	180
GGTGGTGTG	CGGGTCCGA	CRACRTCTT	GCGCTCTGT	CGG		223

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AATTGGGAC	GANGCGGCA	CGTGGGACG	GGCGGCACG	CNGTTGCCAC	CGGGGGGGCC	60
GGGAACGGC	GTGCGGGCC	CGCCGGCGC	GGGGCCGGC	TGATCGGCA	CGGCGGCAAC	120
GGCGGCAGT	CGGGAATGG	CGATGGCGC	GGGGCACAG	GCCTCGGCG	CATCGGTGGG	180
GTGTTGTTC	GTTTGGACG	GGCCAAAGC	CGGCGACGA	CCAACCGCT	GCACACCTGG	240
CAGCAGCGC	GTTCGGCGA	GTCAAGCGC	CCATCCAGC	CGTGACGGG	CGGCGCTGAT	300
CUGCAACGC	CCAACGGCG	CCCGGGCAAC	GGGGCCCCC	GGGGGCACG	CGGTTGGTTC	360
TTCGGGGCG	GAAGGAACG	CGGTTGGGC	GTCCNCRCG	GGGGGGGGG	AAATGCCG	418

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTCGGCAC	GAGGGGACG	ATCGCATACA	GGCTCGGGG	CAGACCCGCC	GGATACAGCA	60
GCTCGGCACA	CSCGAGGCA	CAATACGGCG	TCGGGTGTC	GGGCTTGARC	ACCACGGGT	120
TACCGGCCAC	CAGCGCGGC	ACCGAGTCCG	ACRAGCTAAG	GGTCATGGGG	TAGTTCACG	180
GGGAGATCAC	CCCGACGAG	CGCTTCGGTT	GTAGACACAC	GGTGGTCTTG	GGTATCCGG	240
GGAGGACAGG	CTGTGCTTTA	CGGGGCTTCA	GCAGGTCCAC	ACAGACTCGT	GGTTATAAT	300
TGCGGCTTCC	GGATTCAGAT	CGACCAATTC	CTCTTCGCCC	GGCCATCGGG	CGTTGCGCG	360
CTCGGCTTGG	AGGAAGTCCA	TGAAGAATTC	GGGTTCTCG	ATNACACGGT	CGCGATAGCG	420
GGGATGACT	GCAGCTCGCT	CGATNACGGG	ACCTTCGCCA	CTGGGTCTGC	CGCGCGGAG	480
CTTCGCGGAA	TGCGGCTTGG	ACTTCGCGGG	NCGTGCCAAC	GGAACTNTAT	CACGGGTTCG	540
CGGTTAAAG	CGGTTAAAG	CGGTTAAAG	ATTCGCGAAC	TCCTTATCCC	GGCAGGTGCC	600
AAGSANNCAA	ACCTCGGCAA	GGTTAGGTTT	TCGCCGCTT	YCAAAAATNC	GGGTTTGGN	660
CGAATTTCC	CKGNATGKTG	MCAAGGTTCT	CKAANAACKS	GGGTCTCTTN	NTGNGGGA	720
CGAAAMGGT	TGGGGMGAG	GGMMGCCAAN	CGTACCGCTG	ATRAANGGNW	TTGCGCGGG	780
GGGAKGNGA	ATYCYCCSNA	KCCGCGGGG	GNMCAATTC	TYCGGGMCTC	CTCGGAGTTC	840
WGMGTTTTCC	CAAAAACSC	CGCAATTTM	TTTTTCCTCN	TKTTGANACH	CTTTTCARCA	900
MMCGSAGNS	AMNCCTCTG	CKCTKTGNTK	AAAAAGNAYN	CGCCMAAATT	TYTATTTSC	960
CGCGCGGGN	CCGCTCTTTT	TSCMTTCTH	MYTNCRCMC	MMMSNCKSNG	KKGNGNCCN	1020
CGCCGCTCC	AAATNKGYN	KNTATMAGC				1049

(2) INFORMATION FOR SEQ ID NO:309:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x5) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTCGGCAC	GAGGGGACG	AGAATCCGGG	AATGGTGAAG	CTCGGTGCCC	TGCGGTTAGC	60
CGAAGATCA	GGGTGAGCGG	CGCCCGCGTG	GGATGCTGTA	GGCCACCGGG	GAAAGGGGTG	120
AGGGCTGGGG	TGGAAATPACT	GAAGTTTACT	GGGATGGGAA	ACCGGGTATT	GATATGTATT	180
GGGCGCATCA	AGTTTGTGGG	AATGGGGGAA	GGCTGAGGGG	GGCTGTGTGG	ATTGGGGGAA	240
TTGTTTGGGA	CGACACGGGC	CAGCGGCGGT	GATGGTTTGG	TTSAATTTT	GTGCGGSCCA	300
CANGTGTATG	GGATTGTATT	TGATGGGGCC	SATCGAATA	TTGGGTATGC	GNACGCCSAA	360
CGAGATTGCC	GGGACCTTCA	TGGGGGGGAC	AACCMASGGT	CCSANGTAAR	GGTTTCTTTH	420
ATNTTGAATG	GGATTTCGGG	ACTGTSTGGA	TGSGCTGCAV	MTSATSGGCC	NACNCGMCCG	480
YTATTTTMS	CGTNAVGGGA	ATBAMRGGA	CAAYNTCCCT	CGCMGGAATA	ACCRACMSGC	540
CGCTGTTNCT	CNCCGCGCNC	AKAACCCRTT	KCTGTSTTMC	CGSMAAATNA	CGCCGCGTTS	600
NACTGNCESG	AANTNSCCCC	CGCGGNTT	ATSTYCCGK	GTTCGCCGMC	CGCTTNAAMC	660
TGCGCGGTTA	ACCCGCTTNT	SNCGCCCGCC	YTAAMNCRG	GCTTSTTNTC	CGCCCTTBMK	720
CNCGCGCTCK	SAMCMGNCNC	CTKAAACNAC	CGCKCYGSM	TNCGCAATNT	WCMNCKCGNS	780
KTTNTMTCTC	CGAATVTCRC	CGNCGCTCCG	CKKSSTPCAN	WTATAAAAGC	WCMYAWYNNK	840
KCNMAMATA	MGACWTCNY	WCCGCGNCKX	NTTATMAWCC	CMNCCCKCSW	TCWYCKCSCC	900
CGCTCMMAVC	YCCGCCCKTY	WCMNCCCTTC	CGCCCTCTCG	WCMNBMKCTP	YCSGRTWCMC	960
MYNTMTCTN	CYNAMCKCKX	KTCTTTTTCN	CRNTCTCCCC	CGNCCCGCCV	KKCTCTAKCC	1020
CNMTCTCSC	MMKGGC					1036

(2) INFORMATION FOR SEQ ID NO:310:

(1) SEQUENCE CHARACTERISTICS:

250

(A) LENGTH: 1036 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```

AATTCGGCAC GAGATCATGA ATAGCGGGCT GGTGAGCACC GAAGTGGTCG GCGATCTCGG      60
GAGCAAGTCT CGTCTGCTCG CCCAGCAGGA GGTGGGCATC GATCGGACAC CTTCCGATGT      120
CTTGGATGTT GTTCAGTTGC AGGTAAGGCC GAGCGCCGAG CTTTGTCTAGC AGGGTGTCTT      180
GGCTCTTGGC ACCTGAGGTA ACCAATAACT CCGAGCCGAG CCAACTCCGG CCTTCGATCC      240
GGGTACCGAG CTCGCGCGGA GCGAGCGGTT GTGCCCCCTG GGCCTGAGGT CAGCTGCTGT      300
GCGATCGAAG TAAGAAACCG CGGCATGCCC GTGCGCAAGT ACGACTGACC GAGCAAAACGA      360
ACGATCTGTC TCCCTTCCCT GGGGGTAATC GAGCCGAGCA ACCGACGAGG CCACCAATCA      420
TTGGGATTCG GCGACTGACC GAGCAACCGC CTGTGGGACA CCCCAGCGGA ATTGGTGGTC      480
TTCCGCGGGG CGGCMACCGG AATCANCGGG ACGCGCTGCG CGAASGAGCC GCATANCGCT      540
ACATANCAAC GGMRTCTGCG CCCACATTCG GGGGTMTGCG CCGTCGACAA GSNNAAYNCC      600
CCCATTCTCG AACNAAAAAA TTGGYGCATY ARNGTYCTCM CCAAAAACCN ANTCGCCCTA      660
TCCCCCGGGG GGGGCCCTCY KNNAAAAAGG CCCWHAAGCC CCGGGGCGCC CGGTTTWTN      720
CCCCCTGTGCG GCGCCNCSGG TTTGGTCMCM GGCMMTNNNN GGGTTCGCC CCNCNAAAA      780
AAAAAYCCKG NCAATYAAA CCKCYMAAA ASKTGGSSSC CCGMACCGGG GGAAGGOWNA      840
ANTTAAGCCN KAAAAAANNN NCANNNCCCC NCGGNCCTAA GGGYTTAGGG GTTSTTHANG      900
AAAAAATMTC CANATGSSK TTNHAAAAAA ASCCSWAKCC CCGNRRHNNN CCMAKKAARR      960
GRCCTTCGGG TGGGSGGGG KKKKKTNCMS KNNMMITWGR CCGNCCGCCN NNTTKCCTTN      1020
TCCTNYGNGC RNCAGN

```

(ii) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1060 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```

AATTCGGCAC GAGTGGATTC GATCGAACAC GCGCGCACCT GCGCAGGCCA CATGGGCGCG      60
GCGATGGCCA AGCCTTACTC GCGCAACCGG AATCCATTGG GGGTCTCACC GCAACGCCCG      120
AAAGCGGGCA CCGCGGATG GATCAACCGG CCGACCCGAG ATCGGAARAT GCGTCCACAT      180
AATGAGACAC TGGCGCAAG AGCTTGACAG GCGCGCGACC ATCGCAAGCTG TTAGAGCTGT      240
CGGTCTTCCA AGAAGCGGCT TGGCCACCCA AGATCAGCGC GCGCAAGGCG ATCGAGTCAR      300
CGTTGCGGTC GTATCGCGCT AACGTGCGCG CCGCGAAGAA ATGACCGTGC GCATTACCAT      360
GGCCCCGCTG ATCAGCTTTG GGCACCTGCG CACCANAACG ATGANCAGCG TTATGCGCGAG      420
TCTGTGTGAG ATCGCGAGCC GCTTCAAAAA CTCTCTGTGC ACAATSGTAT TGCTGAGCCG      480
CGGAATCTTT NTCTTTCCAA SAACACTNCA TGTTCNSGGT NRACAACCTY GGTTHGAAAA      540
ACRNCGAATA TTGAANTCCC ANTCGGGGCA GACCONGTTM CGGAAGKTGK TGGGAACGAA      600
TGRTGCCCAA AAATCCCGGG NGGTRAAANW CCGNSRATGG MSAATTTTSC CTNGAACAAH      660
AAAGGTGCCA AGKYCAAAGG NGCCCCCCCC SCNAAATTGG TGAACSCAKA NYANRTTCCC      720
WNTTCAAAAT MTNGGGTGC KNTTCCCTCT AAAGGGGSCN CCGCNCRCGG GNGTGTCCCG      780
NNNNGGGNGN CTYCGCCCA AAAAAAAMMM MTTCGSGKG SWGGKKCCCC CCGGGTYWGG      840
GEYTTTAAAC CCGGGGGGTH CAAAAAANAN ACCCCCCAMS NGGGGGGAAA ATTTGNAANT      900

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AAGGKXKTC	SCMCCCCCA	AAANMMNNCN	ANNCCCCGK	SARGGGGRNY	TTMKAGGMS	960
GRYCCCCCV	YCGGGGGNA	NAAYAAAAGK	NGSHGRGAAT	NTTNTTTTGK	SSSSRNKTTT	1020
TYNTCTCTCN	CONNRRWVG	GRAMTGETS	SSSQQGSGGC			1060

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTCGGCAC	GAGCTTCACC	AAAGAGCTGA	CATGCCGGGT	GATCGGACAT	CGCCTCGGAG	60
GCAATACGGG	CATGGATGAN	CGGAANGGAN	TCTGGCGTTC	GCTCAACTGG	ATTACGCTTC	120
CCAAAGGTAA	ACGCTTTGCG	GCBAAGATG	CGAGCTTAA	CTTGCCCTTC	CACCGTGCAA	180
TGTTNGTATG	GATGCTGGAA	CGGCGCTGAC	NGATAANGAA	TTGCGCTGGT	CGCGGGCAGN	240
ATGGATGCTC	CKSTTTTNC	TCCGCGGTTA	AATTGCTGCT	GCATCATCTG	GCAGGCTATG	300
TTGCGGCTAC	GGCGAGGCC	ATCATGGATG	TGCGGCTAAC	GAANAAGTTA	TGACATGGCG	360
CAAGCGAMTC	GGGCATGCGC	GGGGCAGTTT	CGCAACCTGC	TGTGTGTGAA	GGGTGTCAAC	420
CGAATCGCGG	GTCTAAAGGC	NGGCTTGCCT	TGATTMAAC	CNAACCGNTN	CNATCTCTTG	480
CGNNNNMTG	CTTCTCTTCC	AAGTCCGKGG	SYTGCGGCGG	TGAACCGCMA	CTNCCCGTCC	540
GTGGGACTTA	MTNTTCAAA	ANMCGGNTNA	ACCGGAATNN	SAAAGCTHCC	TCAAANTAMG	600
SAANTCGGGG	TTYGGGNNCC	CCCGGAAAYN	TTCCGCGGCG	GGNTCTCTCN	GGTTTNGGCG	660
GAAACNTTTG	CGCTCTCYNN	TTTACAMGGC	NCMTNNMTTG	GGGCGGNNAG	GNCCCCGGKK	720
TNTTTTCAAN	TGNCKSKTTT	TTXGGGGGGG	GGCGGTCTMC	NCGGGGCGCC	GGCCCCGMAA	780
AAAAAMCMSA	RRCCNYGGG	TCCCGCCCCC	SHATNGGGCC	YKCRARAACAA	ACCCGMAANLA	840
TNGNGMGCGC	SMACCSGNGN	GYNAAAGGCT	TSHSCTMANM	MKGMAANNCT	SGMSCCGNSN	900
NCTCGGGGCT	TTXGNGGARN	AANAMKGGGM	RCGGNGCGNN	GAAAGGGGMS	GGCKSCGNNN	960
NGAANGMCMN	CGNGGJNRCC	NCNGVGMN	NGMNGGNNN	GGGRKNNACN	NMGCAKMSMC	1020
NSNMGGNNNS	CGTNNKCCG					1040

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTCGGCAC	GAGACAANGG	CGTGAATATG	GATCCGCGCG	AGCTGGGGCC	CGTCTGCAGC	60
GACCTGTTGG	CCAAGTCCGG	GGCGCGGGTT	CGGCTCTATG	GGGCTATGTT	ATCTGCGCGG	120
AGCTGTAACT	CAGGGCGAGA	TTTGGGCGGT	TTTCTGCGCC	TGGCTTCAAG	TTCCGGCGAAG	180
TKGGGAACGG	CTAGGGTTCC	CAAGACACGA	TGGGGATGCT	GGGCTGGGTC	CAGGACTGGT	240
ANTCTGATA	TTTGGGTACA	TGTTGACCAA	CTGTGNCNAA	TATTGGGGCC	GCTGCTCGTC	300
NTTCCGCTCC	GGCGCGGTAA	GGTCACACAC	TTCTTTTTC	TGTTGCGG		348

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

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AATTCGGCAC GAGAGACCGG GTGCTTGACC AACGGACGCT TGGGCGCGGG CCCCTTGCCT      80
GGCATACGCG CTCTCTCTTC TTAGCGCCCGT AACGGCTGCG TGCTCTGTTG CGGTCTCTTGA      120
CACCCTGCGT ATCCAGCGAA CCGCGGATGA TCTTTGATGG CACACCAGGC AGGTCTCTCA      180
CCCGGCGCGC GCGCACCAGC ACCATCGAGT GCTCTGCGAG GTTGTGGCCC TCGCGCGGAA      240
TGTACGCGCT GACCTGGAAC TGACTCTGCA CTTCACGCGG GCAACCTTTC GAAGCGCGGA      300
GTTGCGCTTC TTGCGAGTGG TGCTCTGTCG CG

```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```

AATTCGGCAC TAGTGGTCT AGACGGATTC AATGCTCCCG CGAGCACCTC GCCACTGCAC      80
ACCTTGCGAG AAAATGTGCT CAATGTGGTG AACGAGCGCT TCAGACGCT CACCGGCGCG      120
CCGCTGATCG GCAACCGCGC CAACCGGACT CCTGGAAACC GGGCTGACGC GGGGCGCGCG      180
GGTGGCTGTT CGGCAACGCG GGCAACGCGG GGTCCGGGGC GAACGGAACC AACGGCGGGG      240
ACGTGGGAGC GCGCCCGCGG GGATTTCTTC GCACCGGAGC ACCGCGCGGG CCGGCGCGCT      300
GCGACAAAGG CACCGCGGGG GACCGGCGCG CGGTGCGGCG CTTCTGATG GGGCTCCGGC      360
GGTNACCGCG CACGCGCGCG CCGCGGCTCAC CGCGGTGCG GACGCGGGGA CCGGTNACCG      420
CGATCTTTCT CCGGCGCGCG GAAACCGCGG GCGCGGCGCG ACATTAKACC CCGCGGNACC      480
CGCGGCGCGG GCGACCGGCG GGATTTCTTC AACGGCGGGG CCGCGGAACC GNMGGSTGTT      540
CGTNGGSGGA AGGCGCAAKT CCGGCTGATC TTAATCCCGG ANGDKTGAMC CTSATGSMCA      600
MYTMMGGGAA CTNCCCAAT KTTGGRACCG CCGCGGGAAG ASRAWHNGTG KGGCAACNA      660
NNTMCYTTM NATTKGSMNA AAAANCCCTY CCGCGGACT MCCCGCGM GRGMCRTM      720
NTTYYGNCBN CCGGGSNAAM RNTTKATTTC NGGGGGNTCN GGGTMMNNNA AACCCCAAM      780
MERNKSCGA ANGGKSGC NKNPNNGGT TTTYCKMRA MRNWTYNNK NTCNGASRN      840
NAAMCNWSEK NGKNNKAA ARNNTTWTN KNSCNMCM GRNNTVYGGC CMKGSNNNG      900
MCWNHWRNG NNGSCNKC NNGNAAAAA AAGGYNCKS NNMNNKKG NRGGGGGGG      960
GG

```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCGGCAC	RAGAAGACCC	CCGAAGTTT	GGCTGGGCT	TACAACCTCA	TCAAGCGCA	60
GGGGGAACGC	AACCTTCGCA	AGATCTACGT	TCGCTTCCCC	GAAGCGGTCT	GGATCGCCA	120
GTACCTCGGC	GCACCGCAG	GGGAGCTGC	CCAGGATCG	GGCGGAAAC	GGCTTGGTT	180
GCAGAGATG	TGGTTGAGG	TGGCTTGGG	GATTTTGCAN	GGGACCGCG	TGACCGCGAC	240
GGGTTTGTG	TCCGCACTG	TGCTCACCAC	CCGCGGACCC	GGCTTGACCT	CGACCCAGCTG	300
CACCACTCT	GGCCTCTGT	CG				323

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AATTCGGCAGT	GTGTGTGGCG	GGCTCCAGAA	GAAGATGATC	GGGAACATCG	CCAGCGCCGG	60
CCAGGCTATG	GTGCTGGTGA	TGGCGGACCA	GGCATCATC	ACCGGCATAC	AGCGGGCGCG	120
CCGACCCGAC	ACCACTTTCT	GTGACGTGCG	TGGCTTACGC	CAAAGCGTGT	AGACRAACAC	180
ATAAAAGCGG	ACCGTCACCA	GGGCGAGCAC	CGCGCGACG	AGGTTCTGTG	CGCCCATCAT	240
CCAGAAGAAG	GAGATCACCG	TGACGTGAC	CGAGTSCCA	AGCGTTTTC	GGTGGGACCC	300
GGTTCGGCG	CCAGGGCGCG	GGCGCGGCTT	CGCTTCATCA	CCTTGTGAT	ATGCGCGTTC	360
GCNACCACTT	GAGCGTGTG	GGCGCGCGCG	CGGCATCAT	CGCGCGGACN	ANGCTTTTGA	420
GCATGACAG	GGGATGAATG	GGCGCGCGCG	TGGTGGCGCT	CGTGGCGAAT	TCACTTCGCT	480
GNACAACTT	CGGTCGCACT	CGAAGCGCGG	TGAATCAWTC	AATTTAAACG	GGTSAACANT	540
AACACATTA	CGCTTGGGCG	TCCTTAACCG	GTUVTCAANG	GGTTTTTTC	TTAAAGGAAG	600
AACATTTTCC	GGATATGCG	TTTNTWTATC	GAAGAAGCGCC	CGCCCATGCG	CGTTCACAGT	660
TTSCCGCTGA	ATGGAATGCG	ATGCGCTTTC	CGGGGCTTT	AACRCGCGCG	GGTTTTTGT	720
MGCCGCTTCA	CTTTTGTGCG	ATGCGCTTTC	CGGGGCTTT	AACRCGCGCG	GGTTTTTGT	780
TTGCGCTTTC	CTTTTGTGCG	ATGCGCTTTC	CGGGGCTTT	AACRCGCGCG	GGTTTTTGT	840
MAAAGAAAH	GGGGERNGTY	CTTTTGGCGC	CCGAAAGCG	NYCGCGCGCG	YTHRRCMCSY	900
CHTNTGCGH	CTGTCGCGCG	GAARAGAGCG	XCGCGCGCG	STTGTGTWAG	GNRNGKMSRG	960
CGCGCGCGGY	MBDAAYAWN	MBDAAYAWN	STNMAKKN	MBDAAYAWN	MBDAAYAWN	1020
CGCGCGCGGC	CGCG					1034

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

AATTGGGCAC	GAGGCCACAT	CCGGGGCCGC	TGGTGGCATG	ACTCGTGGT	CATCGTGAC	60
RAGGCACAGT	CCGTGGAGCC	CAATGTGTG	CTGACCGTGC	TGTCGGGGT	GGGGACCGGT	120
TCCGGGGTGG	TGTTGACCCA	CGACATCGCC	CAGCGCGACA	ACCTGGCGGT	CGGCGCCAC	180
GACGGGTGGC	CGCGGTGATC	GAGAAGTCCA	AAGGTGATCC	GTTGTTGGCC	CACATCAGCT	240
TGCTGGCGAG	TGAGCGCTCG	CGGATCGCG	CGCTGGTCCG	GAGATGCTCG	ANGAGATCAC	300
CGGGCGCGCC	TGAGTGGCCC	TCCCGCGACC	A			311

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

AATTGGGCAC	GAGATGCTCA	CCCTGGGAC	CAGTGGACCC	AGGCCACGCC	ACCAGTTAGC	60
GCTGATGGGC	CAGAGATGG	ACCAGGTGCT	GTCATGCGG	CCCACCGCAC	TGCAGCTGAG	120
CACCGGGATC	CGCGTCTCTA	GCTACGGCGA	TRAGCTGGTG	TTCCGACATCA	CCCGTGACTA	180
TGACCGCGCG	TCCGAAATGC	AGCAGCTGGT	CAACCGTATC	GAACTGGGTG	TGGCGGCTCT	240
GCTGGCGGTC	ANGGACAACT	CCGTGCTGCT	GTTTACAGGG	ATCGGCTTAA	CGCTTCATCC	300
CGCGCACTCC	CCAGCGCGGC	CGCGCGGGGG	CGGCGCTTCG	TGCGGACCGC	CGGAGCGCGT	360
CAGTGAAGCC	ATCTCGCTCG	CGCTTAACCC	CGTGAGAGGG	TGGGTGGTGC	GCAAGTTGGG	420
CCCGGTGACC	ATCGATCGCG	CGCGGCATGA	CGGCTGGCTG	TTCCACACCA	CGTNGACMC	480
CGCGGAGGAA	CTGGTCCGGC	AMTNCAGGAA	NTGCTGTGTC	GCACGCGCTT	CTTCGCTGCT	540
GGCTTAAACT	TCCNATSTIN	CGCGGGGGCT	CTGGGCTTTC	GNCGGGGGCG	NTCTTTCGAA	600
ATCGGGAAG	ATCCCGACMC	AAACCGCGCC	GCTGTTGGGG	CGCGGGGGGG	GGCGNAGNCC	660
AAACCGCGCC	NTTAAATCT	TGTGTCGCG	CNCGGGCGCC	NCNAGNAGN	CGCTTTGCGC	720
NOTTGGCGCC	CGCAATTTAA	CGGACGCGCN	AAVCCGAGY	TMMKCCCYCY	KNAAAAAANA	780
AATTGGCGCG	CGCGAANTAA	ATTCCCGGCG	CGVTTGGGGG	CGRANCGNYT	TTTCCGNSSS	840
TKGNNNAAGC	NGGAGCGCG	KAATTTMTKG	NAAYCGCGCN	AAMNTTTTC	TAANNCCGCG	900
YNCGCGGAAA	ATTNNAMAM	CGGCTGCGCG	GGGGKTTTNC	GGKGRAGGM	AAAAAANRNN	960
EKTNNCGGNN	SAHNNNNSIN	SGGNSHNNNN	NNNCGGCGYK	CNNANNNCCC	CGCGGGGGGG	1020
CGGCGC						1026

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

AATTGGGCAC	GAGAGAGCGC	CGGAGNGTST	CGCTGGGCTC	TACAACTTCA	TCAARGCGCT	60
NGGGGAACGC	AACCTGCGCA	AGATCTACGT	TGGCTTGGCC	GAGCGGCTCT	CGATGGCGCA	120
GTACTCTGGC	GCACGCGCAG	CGGAGCTGAC	CGAGGATCCG	CGCGCGGAAC	CGCTTGGCGT	180
CGAGAGAGTG	TGGTTGAGG	TGGCGCTGGAN	GATTTTGCAN	CGGACGCGCG	TNACCGCGAC	240
GGGTTTGGTG	TGGCACTGTC	TGCTACGAC	CGCGCGCGCC	CGCTTGGCGC	TGACCAAGCT	300

GCACCACTCG TGCCGCTCGT GCCG

324

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

AATTGGGAC	GANGCGTGGC	GCTNAACACC	AGCCCGGGGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGGCGC	CGGTGGGCTC	GTGCTCTCC	TGACGGGGGC	CGGCGACCAT	AAGGTGCTM	120
ATGCCGAGGT	AGCGGCCGAG	GTGCATGGAG	TGGATGATGA	TGCGACTCTC	CAGCTCGCGG	180
ACCGGGAGCT	TGGATCGGG	CTTGATCAGC	CAGGACCGGT	AGGACAAGTC	GATCGAATGC	240
ATAGTGGGCT	CCAGATGGGC	CGTGCAMTTC	CNGCGTGCTC	CACGGCAAAAT	GGCTTGATTT	300
CTACTCGCGC	TANTGTTGGC	GCATCGGCTG	CGGATGAAT	GGGAACCGCA	GGATGGCGAC	360
GAACGGGTCT	GANTCTAGGT	TTCGCGCTTT	GGGCACAGTG	GTGNACANCC	GGTACTCGGC	420
ATANATCTGG	CCGNAATATG	CGCGCGACGG	CGCCACNAT	AANAACGGGC	ACNACAATCG	480
CGCGCGCGGT	CACGCAACCA	ACANCTTGGC	ATCGGATTTT	GTCCCGANCG	CTCAANCCGT	540
CCCGAACGCG	TGCTCGGCG	NACTTTTCTT	NNANTAAGTG	CGGCTTCGGK	CGCTGGGCGA	600
WTAATGGGA	AACCTTTCG	CCACCTTGAA	GGGCTTGTG	NATTTTACT	GSTAACCGCG	660
AATTTTTCG	GANTCGGTCT	CCCGGGGTTT	YTNNTTGGC	ACCTTGNAN	GGGCGCGCCA	720
AGSTTTTCT	SYTGAAGGGG	GAACCCCAAC	TTTTTTPVN	AACCSCHNAA	MMTTTTTCGG	780
MGAASCONKT	CCCTTTTAC	CAGGGGGGTT	AACCGTMMG	NGGHTAAAAA	GGGKGNKGTG	840
NCGGCTMANG	GGGGGAAAAA	TSTYTCNMG	GGGCGUAAW	ACCMHMTYGN	GTGKKKNGKS	900
GCSAAATTTT	NMRAACTKN	GGGCGCCSGA	NNTTNAAG	MSCCCCNNN	GTGKCGCNN	960
NTTTCNNAA	NMKKGNMNM	SNMISCNMG	GTNKGSGNN	NNAAGMGGGG		1010

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

AATTGGGAC	GANGCGTGGC	GCTNAACACC	AGCCCGGGGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGGCGC	CGGTGGGCTC	GTGCTCTCC	TGACGGGGGC	CGGCGACCAT	AAGGTGCTM	120
ATGCCGAGGT	AGCGGCCGAG	GTGCATGGAG	TGGATGATGA	TGCGACTCTC	CAGCTCGCGG	180
ACCGGGAGCT	TGGATCGGG	CTTGATCAGC	CAGGACCGGT	AGGACAAGTC	GATCGAATGC	240
ATAGTGGGCT	CCAGATGGGC	CGTGCAMTTC	CNGCGTGCTC	CACGGCAAAAT	GGCTTGATTT	300
CTACTCGCGC	TANTGTTGGC	GCATCGGCTG	CGGATGAAT	GGGAACCGCA	GGATGGCGAC	360
GAACGGGTCT	GANTCTAGGT	TTCGCGCTTT	GGGCACAGTG	GTGNACANCC	GGTACTCGGC	420
ATANATCTGG	CCGNAATATG	CGCGCGACGG	CGCCACNAT	AANAACGGGC	ACNACAATCG	480
CGCGCGCGGT	CACGCAACCA	ACANCTTGGC	ATCGGATTTT	GTCCCGANCG	CTCAANCCGT	540
CCCGAACGCG	TGCTCGGCG	NACTTTTCTT	NNANTAAGTG	CGGCTTCGGK	CGCTGGGCGA	600
WTAATGGGA	AACCTTTCG	CCACCTTGAA	GGGCTTGTG	NATTTTACT	GSTAACCGCG	660

AATNTTCCG	GANTCGGTG	KCCGGGGTTT	YSTNTTCCCC	ACCTTNGNAN	GGGGGGGCCA	720
AGSTTTTCT	STTGAAGGG	GAAACCCAC	TTTNTTYYN	AACCCCHNAA	MYMTTTCG	780
MMAASCCNK	CCCTTTTAC	CAMGGGGTN	AACCCCKTNG	GGGTAAAAA	GGGGGINKTG	840
NCCCCNANG	GGGGGAAAA	TSTKTCNKG	GGGGCKAAAW	ACCMGGMYGN	GTGKGNKSS	900
GCSAAATTT	MMRAACTN	GGGGCCSSGA	NNTTTNAAAG	MSCCCCCHN	STGKCCCHN	960
NTTTCCHNAA	MMKCKNNNN	SNMNCSSGG	GKYNSSGGNN	NNAAGMGGG		1020

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

NGNGGGGGWS	NTCAYCAYCA	YCAGGGGGYH	CWATTGGCGG	CCGACWTTGT	MAASAGATCT	60
CGAATTCGGG	AMGAGGGGAMT	CKCTNGCCNC	GCTGTGCAAN	CCAATRAGGC	CYRATAATTY	120
CCACTCCACA	AAAAACGCTT	GTGTGTAYYT	SCCGRAAATR	AAAGGCCCGG	TNTCAACWYC	180
GCCGCTATTT	CCRATYCCCG	THTTGTAMCT	GCCGAGGTSR	AAAYCCCGGG	TGTTGGAYOC	240
CCGGATTGAA	ACTGCGGGCT	TGAAACTGCC	GHTTTGSCRA	TCCGGKWATT	GAMSTCRGG	300
ATTAAAAAAC	CGGKTTTGN	GCTGSHGCTG	CCAAATKGR	AYCCRATAYC	CCATGSCCTG	360
KYCTCTTCK	YCGGTCCCA	AACTGGGTA	TCTTATACTG	GYCCCTAAAK	GCAAWYCKGG	420
GCTGYCMTK	TTGCKGGST	CCNAATTAS	CACCAACGGT	TCTTCCATA	CCNAAACNCG	480
CKTGGGCKCC	AGMCCGAAA	AAAKAATAAT	RAKAAGGOTS	CATNYCCAAA	ACCNCGCCCN	540
CCNANTNCH	ATCCGNTNCG	MSCNCCGCCA	GCGGTNAAGK	TKGGGAAYTT	CTGGRACCCC	600
CAAAACCCCA	TACGNTNCG	GAASAAACCC	CTYCNCGGGG	GYCHNNCAAA	ACASGNTTAT	660
TTGCTCTTT	CGGCMCCGT	GCSCCHNAA	VGCCNAASTA	CITTTTGGGT	CCNAGAAAA	720
ACCNCGGCH	CCMCCSNAA	NWTATYTCTT	KGGCAANCCG	CSAAACCTTE	TCMNAACNCK	780
ATRMTCTCTT	CCCTVSCAT	TGGYCGGRAT	NGGNCCTTY	TCAAAKKKSC	CAKWNNGNG	840
GRNNRACCA	ACCCCAATY	CCMNAAAATH	GKCCGDSCTC	CWACACGNIK	TYTTCSSAAA	900
ASCCWCCCG	CCGCCCAA	AAACCCCCNA	KUUNTCGCA	AAAACNYHKG	GGCCGCCGCC	960
CAAAACAAA	AMCCCCCGM	RMACGGGGGN	NMCCCGCKE	KKTTTCTTT	TKCCMRSCCC	1020
AAGCANNWY	KSHTHMAAA	GGAAGRANCH	TYCCSANAAM	TCCCTYWRW	CCGSGWGMGNA	1080
GAASCCCCC	CS					1092

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GGGGGGGNNH	NATACATCT	SYGTGYACCG	GGGNTYAKT	GGGGGGGGCG	AATCTNGTCA	60
ASGATCTCT	NAMTGGGGG	ACAAAAACTW	GACAAAAYMT	CGMGCMNTEC	GTGTCTCTKA	120
TGCGAAARCG	NGTRACACAG	ASACACRTAT	GTGTCCGAC	CACACATCK	TTGGGACCTC	180
GCTRACCGGY	TGCCCHNACG	CCACGYTGGG	CTWCTATCCG	RACGCGGGGG		240

ATATTCCAGG	CACCACGGCC	AGTTGGTGG	ACAATGCCCT	GGCARTTTCG	TCRAANTTCG	300
TGAACCCGAA	TTCNSHTTGA	AGCCCAAB	CCCCCNCNR	AACARITGGG	NTCCGCGGTT	360
CTCCCCACCG	KTTTCGCGGG	GINTCGGCAN	AANCACACCC	WTGGWTTCM	TCNCCGCGAC	420
GGGCGGACAA	NTCGGGTTCG	AATTTCGCA	AYCGGGGGCG	GGATTCCSCA	ACCGGGGTGG	480
GAAACTGTTT	YCARAAMCCG	GGAKCGGCA	TTTCGGGGCG	AMAAATTCN	YCNACCCACT	540
CTCTTACTT	CCCCGACCGT	AACMANTTG	ATCGTCNTN	CCTCTGCGCT	TGGGCGAGGG	600
CHAAAYACCG	CMTTKGGTTT	CGCAACCTGC	GGCCCAATTC	CCNAMCCRA	CTTTCNATTT	660
GGNTCGAATT	SCCCCCCGGT	RANAACGCC	NTGGCCNNYT	CGGASSAANA	NGGGCCCTNT	720
KGGCNSCCCC	AGTAANACCC	TACCNNAITS	CANTCTTTGC	CAAAATTTGG	ACGAANSKTC	780
GGTTCGCGK	ATTTTPTTGS	GGNCNCCCTN	TATNGGNTN	GGGCCCTCNC	NCSTKTCCKA	840
NASSKAYCCS	NGNKGCGGCT	ACCCCCCTMG	GGGGGTTTTT	NSSGCCCCCC	AWAYGNKSTG	900
GCCCCCNNGG	GGAACAATWT	MWWTMCSGG	GGGAATTTTT	NTSTGGAMCS	SGGACYCCCR	960
GGGGGKTTT	TCCCCCNCSA	NHAWANGGGG	GGGGGAHAYT	NTGNSGNGGG	KMTTITATTT	1020
YTTTTCYCTM	TKACMSGGGG	GTITTKMNG	GGGGGAGAAA	NNAAAAAAA	RAKGGYKNTT	1080
TSKNCACNT	GKNNNNWANR	NAGAGTCTCT	CEKCCNCCSG	SNITTCCTTT	MNNGSGSYGG	1140
GNNGNNNAAA	ACNKRNMMAC	KCSYTYCCCG	CGYCTCCTCC	NCNGGGGYGG	NGSCGNSTYN	1200
GNKKGKNTA	TNTMGNCGTN	SCCTCCNCCC	CGCNENTCTC	TYTTCMYGGG	C	1251

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

AAATGGGAC	MGAGTATCAC	GAATCTGYGT	GGCCCCAGCA	AGTGAGGCTA	TTACTACCTG	60
TATGTGATCC	CTACATCTCT	CTCCCCCTAC	KTGGTCGGGT	GGATGGTGGC	CTGCGCTGAK	120
TCRAAGGTCT	TGGCCRAAGG	GTGATCGCG	CAAAACCTTG	CGCCGACGAC	ATCAKCGCGG	180
AACAGCTGAC	CTGCGCGCGG	ACCGGGGGYC	GNCAATTAAT	CCAAACCGGT	GGCMCTGCTG	240
CTGGCCNAC	CGGTGTCCCA	NTGGGAATC	AGCCGCGMA	CCAKMAACKA	NAAGCTTTGT	300
CTGAAGCCCA	GTTCAAAAAC	CTCAAGTTCG	GGCCCTACTT	CCCGAAACCG	TNCAGATCKA	360
TCBSAGGGGG	CGGGGTGCMC	TGCAACTGGT	TCTTCGNTG	GTRCACCCTN	AAAMCAAGCA	420
CTCGGGGTC	CGMTTCCGCA	CGCGGCCAAS	TTTCTACGG	CGCGGCCNAT	CAAAATTCGCC	480
GGGAACSGSN	CMCCCTCKNK	GGMAACGCC	TWCCAAAACC	CYCAGACCGK	ATCCTTCRGT	540
NMACNCCGGA	RCNCCTCKKT	TCCGGGCTTC	NMGCGGAATA	CCCKNSGMBT	CCGAATCCAA	600
TTACCMKYGG	CTTTTYYVCC	CCCCCGCCCC	AAATYGGGYC	CGTASSNMCK	KNCGRMANT	660
CGMATTCTGG	NGSTCCCNAN	KYGGCGCTTC	NMAATSAMBA	NPNRGGGTTT	TSCYACOMMN	720
AACCGGHWK	KCCCMCKCTK	MANAAAKATT	RATCAMKHWG	GENCKCKCNC	NAAMACCCSN	780
CNCYCNCTTC	TMYSCKKNGC	GCMMYNACCA	SNGGCGAGGW	GGSGGMBGCT	CTMTCTCMCT	840
MGGCCGCTNT	TYCKSGAKAT	ACASMKTTCC	GGCGMGCCGN	MAAMANKAKA	CTAKCCGYGN	900
CGNSTMTYN	CTSHHMBMDN	TCCMMWATC	NTYYGKCKCN	KCTMKATNWC	CGCTSKCKNC	960
NMAATCKTYG	SNMTCCCTCCA	TCMTCKKSC	SNMKNTCKC	KBCNCCNCKN	CNKNCMKCKN	1020
GGNSTCRCRG	TCTGNTNTCS	AGCKCCKGNC	NACNCACACK	NGWCTYTTCC	WONNMCKNKM	1080
TCKCKACRG	NMTFCWCCS					1099

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GGGNTATACA	TCWCTGTGVA	CCSAGGATCW	ANTGCGGCGG	MAAKCTNSTM	CASAGATCTC	60
AAAYTCTGCA	MGAGCGGCGC	AKAKYSTCGT	CCMRACCCGG	CAYACWCGWG	CNCGCCCCWT	120
CTTGGACCGG	GGCKATSMC	ACCGTTGGCC	CCGGCWCSCA	CTTACACCCAC	CCACGCGCGC	180
AGCGCCCCCW	TRAMCAAAAC	ACCGCGCKTT	TACCGCCCCG	GGCGCGGCGG	CCACCACTAG	240
CCCCACCGGG	ACCACCGGCG	CCGCGGTTCG	CAAAACAGGG	CCGCKTTTCG	CACCCA	296

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1073 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

NNGSGNEMV	ATCATGWTTC	TGCACCSNNG	MTGWATTGCG	GGCGCAATCT	TSTMSASAGA	60
TCTCGAAYTC	GGCAGMARCA	TCTCGCGCGN	GAATGTCTCAA	AWGTCTWYTA	CGGCMATCGG	120
TTTGCCGCGA	ACCACCKCTI	SCARATCGCG	GGCAGWYTCY	AACCRATTAT	TGGGCGYCGG	180
AAAATTTCG	CTGTGTACCA	ACCTCGAGCG	GGTCAASCAA	CAGCCTCTTA	ACCTGTAATY	240
CTTAGGTNET	YCCGGCAACA	ASCYORATAA	TSCGCGCGCG	AMCCACAAAA	CCTGANTNGT	300
TNTTNCRAA	NCCGGTYVCC	GRAGGGGTSA	ACTTGCSTAE	GCTTNTCMYC	NCCCTACAT	360
TAAACCCCGG	CGGNTCTCTG	CCGCGCCDAA	ATVCTTSCCC	NTEGCMACCA	YCCDANCCTG	420
CGGTATGGTS	RJANCTATSG	GCRAACGGTM	MCCCTACCKC	TGGCTGATYC	CTCGGNTCCS	480
SNAATTCCGG	GAITTACCGG	CAMGTTTAAV	CCAGGYCCGC	TNTGCTTCKY	CHACACCCSG	540
ATCMWNCNCG	TACCTTKTTAA	AATTCCTTGT	GGTGAACCC	ANYCKAAAAA	NMTNTVCCCN	600
TCCAMGCGGG	CYCGGAUKT	CNACNTGGKT	NACCCCTNCC	VTTGAASITT	TCYTNCCCCC	660
GGCTCCAAAS	ANACCSGAKC	CCCGGAAYCS	WTAGGCTVTC	TGCCCCSTTA	AATTEGHCYC	720
AATCCCKCAA	CGCTCCCCCG	GGTCSGCCMT	TAAAMTTCCC	CCCKSCASNG	GAATYCYKSG	780
GCWGTATTW	CNCCCNCTT	CYKSGMAAAC	SCCCCCWCKG	GCCTYCCCN	SNTTSSGCCS	840
GGTTSGAMTC	AAAATNGGG	MMCNRAGMCG	SGNAMCCSCG	GKKGGGSATW	TRAAATYCYG	900
GGGGGTCTNY	CCCTCCSNAA	AAGYGTGCGC	KCCSSSCCTC	CCMARTTPT	CNGGMRCHAM	960
ACCAAGCGNG	CTCCGCTNCG	WGGCTCCCN	SNMAMAAAN	NKCKCCXGGS	CKGABRMNNA	1020
MCTCSNNGNG	WTCCKXNKC	NSCNESGNCB	YGENSASHCC	VNYCNCACA	ANC	1073

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

CGCCCCGCTTC	TTTMMTTTCAV	TCAATTCACCG	GGMTCTAGTG	CGCCCGCAAK	CTTGCTCKACA	60
GATCTCGAAY	TGCGGAMGAS	AGAATSTCGG	GTGCGGCAAT	GTGNGGTGGG	GCAACTTTGG	120
GCTCGGGAAT	YCGGGGTAA	CGCGGGGTCT	RATGGGTSTG	GGTAATATCG	GGTTTGGTAA	180
TGCGCGGAGC	TACAATTTCC	GTTTGGCAAA	ATATGGGTGT	GGGCAATATN	GGTTCGCTA	240
ACACCGGCAS	TGGRAATTYC	GGTATTSGGT	NACCGGSTRAY	AACTGTACCG	GGTTCGGGTGG	300
TTYCAATACC	GGTAACGGGA	ATGTSGGTTT	TTYACYCCGS	GBAACCGNWT	YTTNGTKCTT	360
TYMNCNTSSM	CKKSAAMTSM	KMGGTSTYCT	MTYCNNGGAS	TAMTYNMCCC	CCGWAYCKSC	420
WAYCCCTCGT	CATYCCMCMC	GGGTYCTCA	MNCACACTTG	NGTYCCCTCC	MMGTTCYCAV	480
CMGTCCGGTN	CTTTCMMNCC	CSGNCRYCTC	AMCNCRTSGK	CACCNATMYC	CSACRCHCTCT	540
MYCYGSCAKN	MTTCCCTCTN	CTTYTNCCCA	MCNCSCTCTM	TGMAACTCCG	CCGTYGCKCTC	600
MYCTCTCTCC	AYNMAACCKK	TYCYWQWYVS	YMYCKCKCAG	WYKMMCTCGN	ACTCTHMYTT	660
TCTCTCNKCC	CMKACCTOFT	CTCNCSCCCC	CCACAKAYMC	YAWCMYTCG	NCTCKACSCC	720
CYYCNYTCM	NMCNMTCMC	TWNAKCANCN	TTCTTCTCTC	MMYMTMACCK	WCHNTCNCKK	780
SGACCTCTC	ACTMKKCCM	TCTCTTMCCK	CCYMWCTCC	MKYNCCCTCC	NMTCTCKYCT	840
CTCTCMMRY	CYYAKCAKCK	NMTCCCCAN	KMCAKCTECT	CCCCCAKMKK	ACNCKCCCKC	900
CTCTCTATCC	NCTCTCTCTY	ATCTCKCTCN	CHYCYMMCMC	CCNCKCYATT	CNACTMMMN	960
CCANCNCTCT	CTNYCTCKCK	ACGTYCKCKK	CTMCKZNYMC	NRNCTYACCT	CKKCCNCCCN	1020
CKNMCKCTM	CTCTCCWMN	TCCCNCCCAT	CTMKKSTCTC	MCNMTCTCTT	CNKCCYNTNT	1080
KCTTYCCMYG	CTTCKNTDMT	MCCMCCYATC	CTMKCCCTCT	CNCACYMCAC	WNTTACWNCC	1140
ACTCTCTCNH	CKCKCMCCCR	MTCTCB				1166

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

NGNGGNMNT	CMTACATCM	TCNACCCSG	NGMTONATTG	CGCGCGGCAW	NCTTGTMAS	60
AGATATCTCN	AAATCGGCAK	ANATGTCTTT	TSTMTAKTGT	GGCGGGGNGC	CACGCKKAT	120
GTATYGCCTGG	GTTACGCCAA	CGCGCGGGRG	CGCGCGGGRG	AGCGCGGGRG	TSAGCGGCCB	180
CGCGCGCGCG	CGCGGTATAT	BAAGCGGCGY	TTTTTKTRATA	ACGGTSCCGC	CGCGCGGTEA	240
TTACGGGCA	AAVCGGKTTT	TTGGGTRTAT	AACGCTAATT	GCAACCAWTT	TTTTYCGGTC	300
AAAAACYCGG	CGMCGCANAT	NCGGGYCMCT	RAGGCGCATT	YMGCGCAAAA	WNTFGGCGCG	360
AAAAACCCCKT	TSYTAATTTN	TGGGGTATSC	GGYTGTCTTG	GCAAACGCTY	CCCGGCTTAA	420
TCCCTCTCCG	GGCGCGGCGN	AAAAACCAAC	AATYCCGYTC	GGGTTGKYCC	CMCAGGCSBT	480
TGCTTCYGMVY	CACCTGGGCCA	AAAYCCCAWT	AKATTTGGGT	GCYCKTSCGG	TTSTYTGGCY	540
CAATTATCCC	CNCGGGNAAA	GRRAAAAANA	ATCNTCONIT	TGCTCGGYCA	YCTTTMTTGG	600
SAAAAAGGGG	ATGGCSGGGT	TYTTTACCT	CAAYCCCGNA	NCANTWACTT	YCCGSCCGCG	660
GGGNCACAA	GGSTTTMGCT	CGSGGNKCC	TGTMCMCCGN	ATCNAAGAGC	CNAGATTTGG	720
TYYSSTYCM	ATTWTWKRY	CCCCMCWTTG	YAAAAAKCCA	AAASAKCCCK	YCNCAWYET	780
NGGGGTYSSG	GCCNTCTTK	SNMTAAACCC	CYCCCCAAAA	YVNSGGGKKT	TCCGCTNSAT	840
KCCACGNCCK	GNCGGGGGNA	SAAAAAAAY	TTTYCCSAAA	ATCCCACTY	TCYCTESTRY	900
AMACCCCTCT	TYMKKAYTC	CKYSCNATTC	SGMTTCWAAA	TYCCGYGGCT	TNTTCCGCCG	960
CGSGNGCCCC	AAATTTGKTT	TYCNANTTYC	CCCNAAHNCM	AWTMGGGGKS	KCCATTCTGG	1020
SCYTMAMNTA	AAANAAAGGG	NKTTTYTCY	NANAAACACN	GTGKCNMCM	CNAANAAASN	1080
AKMAAAKAGN	KKGTGNNSA	AAHCCNCCCC	CTSTYNTYTT	NKTNMCKCC	CYGGKWKGM	1140
SNWSTYTTCT	NCCGCCCCC	YTNKGTANA	AAHNNCYCCS	GGSTMCRNAN	ASNNTTTCK	1200
STSTNGMCC	KMBASHNAN	MCAMWKYCC				1235

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

NGNCGGKRNA	THAYCWTCTC	ACSSGGTCTA	TGCGGCGCAW	CTMGTAASA	GATCTCNAAY	60
TCGGGAMNAN	GCATHTCMNC	CATATATAAC	CATTGCGTCS	GYWTGCANCT	GAAWCTGTTC	120
CTTCGSGCGG	TTKTACRAAG	GTGGMWTGYT	CWYTCCTRAA	SCCCTCRAIC	TCNKTATATC	180
CTKGGGCTYC	ACTTTAACG	HATKSCGTCC	TTXTATCATT	RATGCCAATA	WTGGYCAWAT	240
NTTGCAAGCC	RACGGWYCT	TTTYCGCGRA	GRACATNGA	TTGGAWYCGC	TYCGCRAGCC	300
CGGGCACCAR	ACCGGGCNCC	AAAGGYCCGC	GCAAWTSCCT	GGKTCAAAAA	TGGTGCAAAC	360
AAANCRATCC	CGGYCTTAC	CGCAGTTAMC	ACAAKAAAAA	TCCCTWGGCC	GCACCAWNTT	420
TTYCRATWY	CWYCCGCCAC	TTRAACCTEK	YTGCGTATT	GGCTKCCCTGC	CTCRACAGCM	480
YCNCCCKTCA	AACCTCGCGT	GACTCCAACT	GGTCTGGYCG	AASGGGGGYT	CAMCGGACAA	540
AACCCCRANN	TCGCCAAATT	TTCCGCCGCC	CYCGGGAAAN	GKTGATMTTC	TCSNAACCSA	600
CMGGGNYTN	NAACCTGTAA	CSSGGENKGA	MYNCCCSGGA	ANTTTTCCCT	TYNCGGCGRN	660
AAANCCCTTT	AAGGTACCC	KGGNGGGGKG	CCCTTTGGGG	AAACCAACCT	CKATTGGKTT	720
TGGAATATTT	TKGNCCCCCA	TTCCGGGGGG	GGGCGCCGAC	CCCMCTTTTN	TCMCCNMYTY	780
YCYTGGGAAAT	THYTGGCCGG	GAAYYCGGSM	CCXGYCCTAA	NCCGCMNNGG	GKYSTGSMAT	840
GGATMAWAT	TYSTTTTYMC	CCGGCMNCCC	CCCLAKMCT	KGTTGAAAMA	AAACCGGGGG	900
GCNMYMNY	YNNNGKRTT	THGGSSSMT	TYMAAAMNAN	GGGGGYWTTY	CCNCGSCMN	960
GXTYGGGGST	TTTCCNTTS	GGSSATYKG	MACCCCTCMT	AYCCGGGGGT	NTXTKXCCCT	1020
GC						1022

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

MNCGNNKITA	THAYCWTCTC	NCACCSGGGA	TCWATTGCGG	CCGCAATCTT	STMAASAGAT	60
CTCKAAATCG	GCAMGANCOC	CANCTATTTC	KGTGRASCOC	ACGACCGGGA	CCTCCGSGKT	120
CKTTCCTTCC	AGRGAGGCGK	TGGGTGGCRC	CGGTGGCAAT	GCCAACTGCC	CCCCMAAACN	180
CGGCAATWY	CRAAAACAAA	CCCSGGGOTA	GKTCGSGGCC	GCCAAATMAA	TAACCGTCTT	240
AACKCGAGCN	ACGGCCACCC	GGYCCCGCCC	AGCCAAAGNA	CCTCCGCCSC	NATAGGYCCG	300
GTGGGGGCTG	CKTATATYCC	AATCCTTCAY	CTCNACCGGM	GGGYCCMCWT	TCCGCTTCAT	360
CGGTCTCTCC	TTTMAATTTT	CTCCACATYK	GGGGGGAACY	TTTTTNYCNC	CCTTGGCMAN	420
CACCNAGGAY	CHAAATTTTC	CCCTGCGCTY	SNNCAAAYGR	GATTGGGGTY	GGKTTTNTNT	480
TCNMGMAAC	CGCCNTTTNA	SCCCCNATC	CCVTWATACC	CCGCMNMCNS	ANGWTTGNSA	540
AARTNCCGCC	AAATTCGAAA	MTCTTTCGCC	NTTNTWMCY	YVCCCTTCCC	CMCCGCKAAA	600
GGGCGCGCTY	TCGGGAANTY	TCGCCNCAA	ANTCANWCCM	TTTCCNCCA	AGAANTTCSG	660

SACTGCTTTN	TPCNGGGNAN	ATANATYTTT	YCKTNGGGSK	TTCCGNTCNC	AMMAATNTCC	720
EGGGKAMCC	AGRTTINTCC	YTYTCCGCAA	NMTYCCYKGG	RMCYNNYCY	PTAAANRARS	780
SAACCCSSGG	GKCYNCNCS	TACCCGCCAM	KAAAATTTCC	CCCSSTTTC	TYNNKKGGW	840
GGCCGCSAAM	ACTMTWATTT	TCCCKGCGNN	TTTSYCCCKS	KCAMMGGMTG	SKDCTTTTTT	900
YCSMATAMA	CTTNGGKCT	NTCYNGSGCG	CMMAANAAGG	CCGSGTTCN	TTCCMMACCA	960
YNTSGNMMA	SAAPKAGWATA	ANNNTREKYR	TNNCCCNCC	CKCKCTTSHN	TNCCNCSSES	1020
GGGKPNKKR	GWCTCCWNC	CKCCCNCKNK	CKKWATMCC	CCCSKCCGM	NCCNTTTT	1080
CCC						1083

(2) INFORMATION FOR SEQ ID NO:332:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(12) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GGGGNNKYAT	MCAYCWTCTG	YACGGGMMNC	TATTGCGGCC	GCWYTMGTN	GASAGATCTC	60
GAATTCGGCA	MSAAAAAAGW	GATGTGCTGG	ACCTTMCGGG	CGGGGACGCR	ACCBACAAG	120
RAAGCGCGCC	ANAATATTGG	CCACAKTTGG	TCACATATTT	ACCCAAATMT	AYCAGGGAYT	180
MCCATTGCGG	GGACCCACCG	CACAAATCCG	ATSKTGSTTT	GCRAACGCTR	ACCGTCCGCA	240
MYTYCGCTRA	STTGAACACG	GGCRAAAAAA	CGGCGRAAWY	CTCGCCCTGA	MTCCCGCTCS	300
GGCCNAATRA	CTAGGCCCAT	TEAACGGAAC	CGGNGGCCSC	NANTTGCCCA	ACAGGTCTCT	360
ACMAAGGGGC	GGCASFYCGG	CGGGWYCCG	TTYCACNCCC	TNKTCTCKTG	CGGAATYCGG	420
WTCGATNYC	CGWTGGGGCT	TATCYCKCYK	KYCGGTNCCA	AWCTGNGTA	TNCTATRCKG	480
TCCCTTAAT	GCANATCTGG	GCKYCAATTT	NCGGGNTTC	NATTTAMMAN	SRGCGTTCT	540
TTGWTTCRA	AACCGSNTGG	GGCGNNMCCA	AAAAATGATN	ATAATATATG	YGSCTTTCAA	600
ACCGGGGGG	GGCATTCTWT	CGGTYCCNCC	CGCCGNGGNT	TAAKTTGGGA	ATTTTYTAMC	660
YCNAGGCTCT	MATTTGGGNA	AAAACCTCYC	GGGYCTCAAA	CMYTTTTTTT	GSKSSNTCGG	720
GCTCTTCCG	CAAAACCCAA	ATTNTYRPGG	GGYCKNTNAA	ACMGGGYTCC	RCGGGAAATT	780
TTTTTGTTC	AACGCGAACG	TTTTCAASCC	NTTTTYTYTT	TRCCGSCSMN	TNGSGGGGNT	840
KSSCNTTTCY	BAKKYCCNHN	GGGGGWYCVN	CGCCRMNTTT	CTTTTTTTTT	CGGTNNMAAM	900
NGKTTCTTCA	AASMCCTCCC	SCCCCHSAA	ACCCGCTNAR	GTITTYCHAA	AAMNRYRIGN	960
KNCCTCTCCC	MMMAAAAAAY	YCSGCGGNRN	ACGMSNGGGA	MCCCCCGGNN	NTTRKTTTTT	1020
TWNGSGYCCC	CSMSYTYTT	TKANAMANRR	GAMNSMTTTY	TNNRGNWNR		1069

(2) INFORMATION FOR SEQ ID NO:333:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(12) SEQUENCE DESCRIPTION: SEQ ID NO:333:

NNNGGGGKWK	MATACATCMT	TCTTCAAGG	GCATCATWTE	CGGGCCGCGM	TCTNCTMCAA	60
SAGATCTCGA	TYTCGGGGCA	NACCCACGCG	TCCRAAAAAA	ACCCRAAMCT	CGGCGCTCYC	120
GBAAAGTGT	CGCCGCKTTE	AATTTACAA	ATTCAGTCTC	ANAGTCTCAC	GGCKTTCATW	180

YCCCGGCAAA	GGGGCCACAA	CGTGCAGGA	SCACYCRATG	GKTYGTYGTS	CNCGGGCGGG	240
CCGGGTAAAG	GGACCTGCTT	GGGKTGSCC	TMCAAAATC	NYCCGGGGGT	YCGCTGGGAT	300
MNCGAGGGGT	GTCAAAAAC	CGCAACAGG	CACSCCANC	NTTTACGGGS	CTTAAAAAGA	360
AAAAGGGGTG	ATGCCCCCAA	GGGGGGCCCG	NCCCAACTTT	CGTTTGGTCA	ACAACCCGGT	420
CTCTCTCGCC	RAATCGGWT	CCRATNYCM	CNTGGCCCTK	TCKYCTYCTY	CGGTACCCAA	480
ATCTGGGTAT	CCYATATGTT	CCCTAAWTT	CCAAATCTGG	GTCTGCGATT	TGCTTGGCGT	540
TCCAAATTTA	CCANCAACGG	TTCTTTCAT	NCCAAAAACC	GNTTGGGCKC	NKACCCCAAA	600
AAATGAATAA	TAATAANNGG	KCNWTTCTA	ACCNCGCCCC	CCCNATTCCA	TYNGTTTCCA	660
NNNCCCCCAG	NGGCTAGGTT	GGGAAANYTC	TCMACCTYCA	ANCCCTTARS	TTTTNGRAAT	720
AAACCCCTYC	YCGGGGTGWW	TYMAAAAMA	NTTATTTCGG	NGNTTTCGGG	MNCKRKGNT	780
GCCAAATCC	MAAATANTTT	YTTGTYCTGA	TWAAAAAMCG	YGNCCMGCCC	GGAAAAATTT	840
TTTTGKTTSA	ACCCCAAAAC	YTTTTCMNAA	NCSSKTTTTC	CTTTCCGCCC	AMNTTGGGYS	900
GGGNATGTYG	SCYTTTCTTA	TKTCTYMTW	CMGGGGGGNN	MMTTCMCCC	CCMTTYYCY	960
NYWTTTTFTN	KCCCCCTNMR	NHRAAHNGN	YTCGYNAA	AAGCNCGCCC	SCCKNCCCA	1020
AAAACCCCN	NHRAUKNT	TTMKANRNM	SCCKNKNGY	YCCCCCCCWC	YNNNAAAAA	1080
AATMYCCNC	RASANMCASH	NMGGRGNRC	CCCCCCCCST	NNNNNTTNT	TTTTTCSRA	1140
GAGCKCCCG	MGUANMKCK	CTTTTCKNC	NNNNNNNN	GGNGMCKCC	CCNAGAAMWE	1200
CTKSTCCCE						1210

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) SEQUENCE DESCRIPTION: SEQ ID NO:334:

NGSSSHGNA	TMATCTGCTT	GYACGGGGT	CMATTGCGGC	CGCAACTNGT	MAASAGATCT	60
CGAATCGGC	AAKAAACCC	ACCCCGCTGT	MTATACACCG	CAAAATTTCT	GTATGCCAAR	120
ACCGAGACGC	CGCGGCGCG	GGGYTCCAAC	CGKTTAGYTR	ACCGCGCAGY	TCAGTTGTTA	180
AACCGTGTGT	RAGGGCGCGA	CCCAACMTAA	ACGCTTTAK	CAAGRAWTGT	GKTGGCCGCG	240
AGCCACCTGT	TGTGGYTGCC	CTCWYCGGTG	GTAGGCGCGG	TTANCGCCGG	TTGCGCGYTC	300
AMCASCSCGC	CGGTRATCCC	AKCMWTCGCC	CGGCMRACC	CMCGGGCAC	TTTGRACGGT	360
GCTGCCAATT	CAAACTGCTT	GRWTCCTTC	AAACACACAC	AAGGCCACCN	CCMSCACCA	420
ATMGCGRAC	TTAAGGACCA	GGCAAAACCT	NTRAKCMCTT	CCCGGCGRAA	GGTCCGCAAA	480
SCRATCMMA	AAAACKXNAT	TTCCCGKAGC	AKCAACCTAA	MMCGSTTTGC	TGCTTCCGGA	540
TTGAAACCA	ATTTCNGGKT	MCMGGGGAAA	AACACCMNCC	NWTAACCMGG	CCCMCGGACA	600
ATTTGGRAAA	SAACCCCTNY	CCCGGGTTTT	YCTTGCTCMG	GCOCANACC	CCCGGGAATC	660
AAAAAGGTC	GGNCAAANGG	CGMAAACCCS	SACCMACTT	WTTCCCTCTN	GGGGGGGACN	720
CCNCTTTAA	ANKSCCTNY	CTSCCAAAAY	TCGGGCHAAA	NNRKTGTGGK	TTNGGCHACC	780
NTTTCGGKRC	CCGGGCKGKE	WGYCTGMAA	CTTTNTTTTT	SCCCYKAAA	NYSCCCCCCC	840
CGSSSCCCCC	CCCGGGGGGA	NNTTTTTAMA	GKTYTCCCTT	CCCCAMAAAA	ANACCCCNCT	900
CCCGGCGCCT	TTKRAAAAMN	KCTSCCCGNC	GNNGGGGCKM	GGKTTATTMT	NNNCCSCCCC	960
TCCGCGSAAA	AAATATNTTT	SYCCCCCNC	CTCCCKNMR	GKAMSNCCG	TCCCTCTCNC	1020
CGNCTMAAN	ARSNCTGNN	CNCYKCCG	NSNGCKNWD	NCCSTSNCT	NKGNCKNWN	1080
KAAANAAYNC	NGSMSTSSMN	CNKC				1100

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(14) MOLECULE TYPE: Genomic DNA

(14) SEQUENCE DESCRIPTION: SEQ ID NO:135:

NGNSNINQNN	TAMAYCWYTC	TSACCSNGGA	ACHANTGCGG	CCRMHWCTNS	TMKASAGATC	60
TMGAAYTCGG	CAAGAGCGGC	AAGAGTGTGT	GCATCTGGTC	AMAGTSTHMA	CRCGGTGCCG	120
CGGGTGGGTR	GASGACMCAT	NTGCGGRACAC	CAAGCCCTTC	CGGGGYCACG	GGCKTGGCCT	180
GCAGAAWYCC	CGAGGCCACC	TCAACACAYW	YCTYCTGCAA	CGCARGCGGT	TYCGCGGGCG	240
RATCTTGKRT	CASYTCGCTC	TGCGGTGCCC	AAGKTACTGG	CGCAYCAAAA	CGGCTCGGGG	300
RAACRAACKT	AAWYTCGCG	AAITTCMTTC	CGCTCGGCTT	TGATAAAAT	NTNAGAGCCG	360
CGCAAMCCTY	CGGGCTCTTC	CTCCTGCCRA	ATYCGRATCC	RATAYCGCCA	TGGCTTMTTC	420
KYCTYCKYCS	GTACCCAAAT	CTTGGGTATC	CTATANTKYC	CCWAAANRCA	ANTCTGGGCK	480
KTCCATKTC	TGGGSHCCRA	ATTYAMMACA	NCGGTTTCTT	TCTACCCAAA	AACGNTGGG	540
CCCCACCCCA	AAAAAGATAA	TAATAAGTGT	CWMCALAAAC	CCGCCCCCCC	RRTTCAAYCS	600
GTCCARCCCG	CGAGSHGGTN	AGGTNGGAAT	TYTMAACCCC	CAGCCCATAA	SHNTNSGMAA	660
AAACCCCCCN	GGGYMYCAAA	AMCCTTTTTC	GGGMITCSGS	CCATKGYKCC	AAAACCAAAA	720
TMTTCCTGCT	CRHAAAAACC	GGGCCMCCCG	NAAATTTTTC	GKCAACCCCA	AACCTTMMAM	780
CCMNNTTCY	YCCCHACAAA	TGGGSGGGGN	NGSSCNTTTC	TWTTTYNNNA	GGGGGGRRNC	840
SHCCCCNAAN	YYCCNAANNG	NKCCCGGSHM	AAAGAGANTT	YCMKAAAAAC	CCCCCNCCCC	900
MAAAYACCCC	MAAAWTTTCM	AAASMSCHNG	YCCCCC			936

(2) INFORMATION FOR SEQ ID NO:335:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1042 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(14) MOLECULE TYPE: Genomic DNA

(14) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NNNNNNNNNN	ATMMAYTCWY	YCTSCACCCG	GGNNMCWATT	CGGGCCRMHW	KCTTGTMAAS	60
AGATCTHMAA	YTCGGCACAG	ASSSGCACAG	ASCCCGGGCG	CTATYCMYCC	GTTGCTCATG	120
CTCACACACG	TCKTCGGCGW	GRATAATGGC	NGCGCCGCGG	CGCCACACAG	YTCATYTGCT	180
TGCGCAACCG	CAATNTTCAA	CAAGGTRATA	AAAGCAAAAC	CGCGCGCCGY	GGCCTTGGCG	240
CGCGRAACGG	GTGCCAACCG	RAAACNCMTT	GGGCKCYCGG	KTSRACTTAA	ASGGTAATC	300
TCKTCTCTCT	GGGTATGGT	GGGCCACAAA	CGTSTYTGCG	WGGGTCTGCG	CGTGGGYCAC	360
GGYCRCTTTC	TATNTMTCK	YCTACACMCT	TGNTYCAAC	CAACCCACTT	CACGAAATTC	420
TCTTGGGCTT	GGGSGCCCGG	YGTSTNCCGK	TAATAATCGG	NTGTCGCGCC	MYCACCGGMA	480
CGATANGCT	CGCGGCGCTG	GCAAAATTCG	SAATCATYTC	CTTCTGTGAC	CGCCACAMRC	540
CTNSAAATCC	GRATCAATTC	CCCNKGGCTT	NTGYCTCTCN	GTRCCCAATY	TGGTTCTAT	600
RKTNCCCTAA	TSCTAATGGG	TTGCCRTTSC	YGTSTCCAA	KTTACAAAGS	GGTITTYTCT	660
ACCAAAACCC	NTGGSCCNNA	CMHAAAHANA	RAAAAMAKGG	CTTHTYAAAC	CCCCCCTAT	720
TCAWYCGGTC	CGNNCCCGCG	NGKAAGGKGN	GAAYTTTTRA	CCCAANGCNT	ABSTTSGNAK	780
AAACCCYTCG	GGGTSMCAAA	MKNTYTTTSC	CTTCGGMCCT	YCCAAATMSA	AAATYTTCKK	840
ERHMAAAMC	YGNCCGCCAA	AMATTTTGTG	NAAMCCCKGA	YXRTTMMCK	WTITTCGYCC	900
CCNKNNSHSG	GNTRCCCTTY	TYATTTTCNM	MCNNSHGAON	CGCCBTFTTT	TWITCKKCMN	960
MMARGSNNTT	RGHMMNMNCC	CCNCCCNNAK	MTCCNCAAAK	NTTTHAACGN	NNEYCKCCCC	1020
CCCMNNNNCC	CCCMNNMTT	TM				1042

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

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NNSSGSGNKK ATAMATONCT CTSTACCGNG GHTCWATGCG GGGCGMAMTC TNGTMAASAG      50
ATCTCGAAYT CGGCAAAANAK ACGGMAVGTG AAGTGTRAVY CGGTCCACATA TONTGCGGNG     100
TCAACMCCAA AGCCGNGTCA CGGKCTCCCT GGGCGGCCAC CGCCATCGGT RATGCAACTT     150
CGGCGGCCAC CGYCAAAAGG ZTCMTTRAGG CGCTAAAGGT CAMCAATTCC TRAGGTTCNG     200
CACCGTNTTT TGGCCGCGCC RANTYCTTAC CGGCAATWTC GGTAAATCGGR AATTGGGCGN     250
TCGGCTTGGG CAATAAGKTN TGGGCAACG CGGSEWTCYC NCTGGCGGGA ATTCGNCAT     300
TCTCTTACG GKTGACCGT TTYCCCGYT GCGCTAAYTG TTYCTGGGC GCGYTCGGCC     350
CRNAGGASYY CRTCAACGGY CMCCAGSCAA TACCKTGGC TTTAAACCA CCGGATNAAY     400
TGKTAACGAC YTCASSGTS CTGRANTTRE THTCNTGAAA AANMCCACCN AACCGGNTT     450
RATCTGCTTC MTCANOWTT SCGSGGTTCT GCGCTTTTGR GCGCTTTNATC CMYCAAAAG     500
GTTTAMTTC CCAAMRAAT CGGTTTGCCA GCTTGCGCGG GCGTGGTTM CGMWCCTTRE     550
AMATGNCNCS GCGGSAANAN AMTTSGGNTT GCGCCGCTCC CGCGNAATAT YNTGNGNCT     600
GNAAAATGSG GGGATCCCGN GSGNAYCGGG CGWTKGGGK TNOCCACGTG GWACAAATTYC     650
NKGCGTTCGA AACCCGGGNC CGGGGGGTGG GSCCNITTT COTMYNAAA AAGKSTTGN     700
NYTSTTTGCG CIRAANITCA CGSKCKNTNT GCGCENACY YTYCAANTYC CAMACTTTTA     750
AASAAANCYK YGKTYCGCC TTTTMCSSG SANCGCCCG NMSSKNCGGG AAAAAAAGHK     800
TYNGCCCTAN CINSNTKTT TTKTYCCCC NMNNNSMICY NCBKCKNERY NGNSNNSCTT     850
MKYSKCNMNN SNNNNNKGCG GNCSCGMKYM CNMNCNGMFK NGNKNNNCCC MSC           1073

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(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

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GNSNGKNTN TMCAYVWYCT SCACSGGCTC TATTCGCGCC GCATYTYNGT CKASAGATCT      60
CGATVTCGGC AMNANAARTQ TCTGTGTCAA TTTCAGKKTG GTCKTCAAAAY GGGCCAGGCC     120
GNGACCCACA CCGTGNSTCA CCAAAAANAC CAACAGCWTG AATWTCRAG CGCCAGGCSG     180
TRTCAATYCC CRASCAKTTA ACCGTKTCCW TCRAGGCTGC CRAACCAAGG ACCCGYTTCA     240
CCGCCSGGCA AMTGGGCGTG CGGGCGGGTN TCAGCTTGAT TYCTGACCGT SMTCTGTSGG     300
TGGYCAMCNT GGTGAAGGGC CWRCCGCGNA AGAAGTGGAG GGCRAATTCC CAGGAGCCNA     360
GRAACCCNAG GAACCCGCGG TAAANCCCG CRAAACCRAG CGCGTGGGCG ATTCGNATTA     420
NAMSGGTTTG CRACMTGGCT RAACGTTTTT CTGCTGCGGC CTGGGCAACC GTGGACCAAT     480
TACCCCKTNC CGGCMCMAC CYCGGTHCT TGYVCCCAAT NTGTCYCCCG GNRANTNGGC     540
CNAATTTCCAG GCGNCACANT TCCGGCGGCG AATTCCGYTG GTTAATCACC GCGCNGNCTT     600
GGTTTTGGGC AACCCGCTY GTTMTTAAA CATTCGCGCC CAAATGGGNC STTGSSAAAT     660

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TCNTNYCGGT	GGGCGGGCC	AMMYTTCTCT	YCCMAAASAN	CTTANYCCAN	TTGSSNTCC	720
CGGCKAAAS	NGGGGGGGA	AAGGGGCCCC	CGKNTSCKCC	GGGCKGCCCC	CYGGKTTCAA	780
AANTTTCSGG	GETSTMBGG	NVTCSCCCCC	CSGCCAAGRA	CCONGGTTTT	TTTTGAACC	840
KCMATCCSA	AMCCGCCSC	CCMAAAGGS	GCTNAANGR	RAYTTNKSCC	CNNAACSGG	900
CCCCCAKTY	SGGKTTCNC	CHCCSGKGT	CMSTTTTMM	MRCCCTTTGN	GNKTTTAN	960
MGSCCTTNC	CACCCCTCK	GGGCKSMINA	GAATMYKCC	CNGGCGNNAN	RSCCCCCN	1020
GGGCGGGGG	MGAGYSCKT	CTGCGCNCN	YKNTTCCCC	C		1061

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 995 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GNNGNNNNNN	ATMCAYCNY	CTGCACCGG	GMICWATTGC	GGCGGCANWY	TNGTHAASAG	60
ATCTGAAAT	CGGCACANAG	CGGCACAGAG	TGTGTGATC	TGTGTGATC	CTGTCAACGC	120
GGTTCGCGCG	GTGGTTRAC	CMCATTCGGR	AACACAAAC	CGGTTCGCGG	GYCACCGCG	180
TGCGCTSCAA	AAYCTCTCG	GGCACCCTCA	AACAAYNYCT	CGTGCACAC	ARGCCCTTC	240
GGCGCGGAT	CTGCGCTCA	TTGCGCTGC	GGTGCACCA	GGTACTGCG	GWYCRAMCC	300
GGTTCGCGG	ACGNAACGTA	AATCTTCGCG	AAITTCGNTT	CGCCCTSCCC	TTATNAATT	360
TGTTAAACCT	CGCAAACTCA	CGGCKCTCT	CTCTGCGCA	WTGCGRWTC	RATNYCGCCA	420
TGCGCTTNC	KYCTYCTCK	GTMCACAAAT	CTTGTGTATC	TATATTGCTC	CTAAACGCAA	480
ATCTGCGCTG	TGCAATTCGT	GGCTTCGAA	TTWAMANCAG	NGGTTCTCTT	CTTCGNAAC	540
CGCTTCGCGG	CAACGNAAC	AATGATWATA	ATRAATGCTC	TNTCAAAAGC	GGCNGCCATT	600
CNATCGKCC	AMCGCCTGCG	GGTATNCKG	GNATTCCTMM	AACCCCAAGC	CATAGSNTTG	660
GGNAAACCT	NCNCGGCTCA	CCAAACAN	NTNTTGGNT	SSNTTGGGNN	YCAGGCTMN	720
CMAAAACCT	AATACTNYTC	GGYCAATAA	AAAMGGGYC	SAMCGGGA	NTTCTVTGN	780
KYNAACCT	AACCTCTCT	CAACGCTAN	MTYCTCTCC	RCBMAITGG	CNCGGARTXT	840
SSCTTNC	ATGKYCTMA	AGHGGGANA	CGACGCGCA	TTGCTTNTTN	KYNGCCGNT	900
TRNAAAGG	GGTNTGMA	AACGCTTCC	NCCTTCCCA	AAKAMCCCN	AAAGAKNTCC	960
MAANAKRYN	NNNCCCTCC	CTMMN				986

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1974 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

NGNGGGGNN	ATMMAYCCT	SATYVACGNN	GGMMGATTC	CGGCGRMAWT	CTNGTHKASA	60
GATCTGAA	YTGGCAAG	AGYATCTCG	GGGCGCAGAT	TTNTGCGCG	CAACGCGCG	120
ACTTTCGAY	TCAACATCC	GGGTGCGCA	AAAAATCTWT	ACCCCATATC	TYCTGTCAM	180
ASSTTGC	RATTACAC	CGGCGCGCG	TGCTGCGCG	GATATTTCAS	CAGTTCAAAY	240
YCTTCTAGK	TAAATCCAG	CGGCTGCGCA	CMACGCGGG	CGGTETAGGT	GGCTTCTCA	300

ATMACCAGCY	CGCCGAGGY	CACCTTGGCC	AAAAYCTCCT	GGGTGAGCCA	AATTTCGGCS	360
CGGGCCCAAC	ACGACGCCA	TYCTGGCTTC	AATCYCAGCG	GGCCCGGTGY	TAAAMPASMA	420
GRATCTCTC	MANCCCCAN	TCAGGCTTNA	CNGCMACAGC	CGGCTTCTT	CAMACGCCA	480
RTACCGGWT	CAACCGGCC	GTCAAACTCA	ACAGCGGCGC	AGGCTTCCCC	CGAASAAAG	540
GTCTTACGC	NNYAAANAAA	MAAGTCTCT	TTTCCCCCTC	CASAAANAAA	AAACCCCGGC	600
CGGGCTCTCN	NNMGGGTTTG	GGGMAANAAA	AARCCCGGNN	GGAACGATC	CGAAAMCTCC	660
CAAGTCNCT	TWANAACYCN	KWAAACCCCC	ANTTTTGGGA	AAGGNTCCCC	NTMYTCCCCC	720
TTTTAGGITS	GGGNNYCTY	TAAAAAAAT	CCCCAAAAG	CCCCGGGAAG	GGTCMACTCG	780
GGNAATTTT	CAAMCCNMGK	TNTTYNGGT	TMCGGGGGRA	AATTTCNCTC	CCYTNNGGGS	840
CSGGSNRNAT	DAYGGSNMNT	TTTNNAAWTM	NSGKTSAMM	YNNKCCMNHN	SNMMSMAHKK	900
TNAMKCCCC	CCTCNGNGKY	CSYKCCGCS	GNAGNGGRAS	KKCCNANMAA	AYASGTTNKK	960
CGGAAMCCNN	AATGNNNNSC	CCGGASMCNN	NNNMAAATMT	CNCKNCKSNM	AANKMPACIN	1020
CCCNNSNGMN	REGAARMNTY	YCCCCGGSKM	GKGNKAAAW	GKYCCCCCCM	AAAG	1074

(2) INFORMATION FOR SEQ ID NO:341:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

NNNGNNGNNT	MTACATCWT	CTGACCCGG	GNTCANTGC	GGCCGCAWKY	TTGTGASAG	60
ATCTCGAAT	CGGCAMGAG	ACWCTCCRA	CGCCCCDACA	KACTCTGGCG	TGTGIACCC	120
ATTGNGCGK	TCAGCGCGCC	ATGACCCAK	TWACTCGGK	TCCCGTYCGG	CTTGGCGGCG	180
GGCTCTCAG	CKCTCCTCT	RAAGGCTTG	CGCAGCGCAT	TGGTTTCTCT	RAACGCTGGG	240
AAANTTGGCA	GGCTCTGGC	TCATGGGNTC	TACGCAACGC	CNGCCCCCAA	CRCTTTCTTA	300
AATCCGKYCC	NTCCGAGCS	CTTTGAAVCC	CGGGGSAAGA	ACTGGTTGCS	CNCGAYCTCG	360
TGGAACCTTK	TGNAATCCC	GCNAKTGTT	TCTTAMGYCC	CNCCGGGAAG	NGAACCTACT	420
TTGNGWANG	TGGGCKKCCG	CGCCTTATCA	CTCTGATCA	ACGGGGAAC	GGYKNNSTTG	480
XGGGAAAAAG	RECCCTCAATG	MTYGTCTCC	GCTCGGKANC	CGCCCCCTGK	GYCCGNAATG	540
GAAGGCSMAG	GGTTAANCC	MTTYCYTCR	RECCCTTGA	GGKNTTYCGG	MGGANAKMNN	600
NNQAMWTTK	TCGNGGGCCN	ATSTCCGGG	CESTTKAGA	ANACTYCCCK	WCCSTNTYSC	660
SAAGNTKCS	CGGCTTTTTS	CCGKMGANGN	YCTGATTTSA	GGGGGKYKCC	CCCCGGGTTC	720
CGAAWNNRY	CTYAGGGGGM	GGYCCAGCSC	CGMNNATNAG	AGNAAGGKTT	RYGTSTSENC	780
TYTNAGGACC	WCCNCHMSAK	ANAAACNNKT	TCCSCNTMS	AGNKTINKGT	YCCNKTSTTC	840
TAAGAGGAGC	TATKMKCGCC	CKTGGAAGM	GAGMNGGCG	HYCCCSNKRT	TGNTGMAAA	900
TATKASMGAG	TKCCGMAGMK	CCSCCTTTKT	TRTGANAAMN	MSMKKCKKTK	CGMGVCTCTCT	960
GGGNTTTGTA	GAGTAKTCGS	CCSCSMWAGC	WCSGCMGNG	AGKNTKNTTS	YANTGARGCG	1020
MNNKTKMKT	MSCSCCGGNA	GGAGNGCCCC	CGANGMTGY	MEGGMNSNG	ARAKGATGGS	1080
GGCCNCGMN	MMMGGAAMGA	SANNGMCGMR	GGGGGKTGK	TKKCSGCGNS	CSANERAGAA	1140
GKTCNGSCGC	CGMGKYCKT	KTKTKKTKTG	YSTCNSMNM	NAGAAAAAGAG	AGGGC	1195

(2) INFORMATION FOR SEQ ID NO:342:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

[x1] SEQUENCE DESCRIPTION: SEQ ID NO:342:

CCATCTGATC	GTTCGGCACT	AGCATCGCAG	TGGGAACGAT	GCCTTCATTC	AGCATTTCGA	50
TGGTTTGTTC	AAACACGGAC	ATGCGACTTC	AGTCGCTTC	CGCTTCGCTT	ATCGGCTGAA	120
TTTGATTGGG	AGTGAGATAT	TTATGCCAGC	CAGCCAGAGC	CAGACGCGCC	GAGACAGAAC	130
TTAATGCGCC	CGCTAACAGC	GGGATTTGCT	GTGACCCAA	TGCGACCAGA	TGCTCCACGC	240
CCAGTCGGGT	ACCGTCTTCA	TGGGAGAAAA	TAATACTGTT	GATGGGTGTC	TGGTTCAGAG	300
CATCAAGAAA	TAACGCGGGA	ACATTAGTGC	AGGCAGCTTC	CACAGCAATC	GCATCTGTGT	360
CATCCAGCGG	ATAGTTAATG	ATCACGCCAC	TGACGCGTTT	CGCGAGAAGA	TTGTCGACCG	420
CGCCTTTACA	GGCTTGGAGC	CGCCTTGTTT	CTACCATGGA	CACCCACCAG	CTGGCACCCA	480
GTTCATCGGC	CGGAGATTTA	ATCCCGCGGA	CAATTTTGGA	CGCGCGTTGC	AGGCGCAGGT	540
TGGAGGTGGC	AACGCCAATC	AGCAACGACT	GTTCGCGCGC	CAGTTTGTGT	GCCACCGGGT	600
TGGGAATGTA	ATTGAGCTCC	CGCATCGCGC	CTTCACITTT	TTCCGCGGTT	TTCCGAGAAA	660
CGTGGCTGGC	CTGGTTGAGC	ACGCGGGAAA	CGGTCTGATA	AGAGACACCG	GCATATCTTG	720
CGACATGATA	TACGCTTACT	GGTTTCACAT	TCACCCACCT	GAATTGACTG	TCTTCGCGGC	780
GCTATCATGC	CATACCGGGA	AAGGTTTTCG	GGCATTGGAT	GGTGTCCGGG	ATCCGACAGC	840
TTCTGCTTAT	CGGACTGCTG	CATTAGGAAG	CAGCCGAGTA	GTAGGTTGAG	GGCCTTGGAG	900
ACCGCGCGCG	CAGGGAATGG	TGCATGCAAG	GAGATGGGCG	CCAACAGTCC	CCGCGCCACG	960
GGGCTTGCCA	CCATACCCAC	CGCGAAACAA	GGCTCTATGA	GGCCGAAGTG	CGGAGCCCGA	1020
TCTTCGCGAT	CGGTGATGTC	GGCGATATAG	CGCGCAGCAA	CGGCACCTGT	GGCGCGGGTG	1080
ATGCGCGGCA	CGATGCGTCC	GGCTTAGAGG	ATGAGAGTGT	CGATCCGCGC	AAGTTAATAT	1140
GACTCATCAT	AGGGGAATTC	TGAGCGGATA	ACAAATTCGC	TTTGAAGAATA	ATTTGTGTTA	1200
ACTTTAAGAA	GGAGATATAC	ATATGGGCTA	TCATCATCAT	CATCACTGTA	TGACATCATAT	1260
CGCGACGAGC	CGACATATCT	GGGAACAGCG	GGCGCGGGAG	GGGTTCGACG	GGGCGCGGGA	1320
TAGCTTCGAT	GACATCGGCG	TGCGTGGGTT	CATTGAGCAG	GACATGGCCG	TGGACACGTC	1380
GGGCAAGATC	ACCTACCGCA	TCAAGCTGGA	AGTGTGCTTC	AAGATGAGGC	CGGCGCAATC	1440
GAGGGGCTCG	AAACCAAGGA	CGGCTTCGCG	TGAAACGGGC	GGCGCGCGCG	GTACTGTGCG	1500
GAGACGCGCC	GGTCTGTGCG	CGGTGACGTT	GGCGAGAGAC	GGTAGCACGC	GTGCTTACCC	1560
GCTGTTCGAC	GTGTGGGCTC	CGGCTTTTCA	CGAGAGGTAT	CGGAACGTCA	CGATCACGCG	1620
TGAGGCGCAC	GGTTCTGGTG	CTGGGATGCG	CGAGGCGCGC	GGCGGGACGG	TGAACATTGG	1680
GGCTGTGAGC	GGTTCTGTGT	CGGAAGGTGA	TATGGCGCGC	CACAGGGGCG	TGATGAACAT	1740
CGGCTTAGCC	ATCTCGGCTG	AGCAGGTCAA	CTACAACTGT	CGTGGAGTGA	CGGAGCACCT	1800
CAAGCTGAAC	GGAAAGTTCG	TGCGCGGCTT	TACCAAGGCG	ACCATCAAAA	CTCTGGACGA	1860
CGGCGGATTC	GCTCGGCTCA	ACCGCGGCTT	GAACCTGCGC	GGCACCGCGG	TAGTTCGCTG	1920
GAGCGGCTCG	GAGCGGCTCG	GTGACACTTT	CTGCTTCACT	CAGTACTCTG	CTCAAGCAGA	1980
TGCTTAGGGC	TGGGCGAAGT	CGCGCGGCTT	CGGCACCACT	GTCCACTTCC	CGGCGGTGCG	2040
GGGCTGTGTC	GTTGAGAAAG	CGACAGGCGG	GGTGTGAGCC	GGTTGCGCGG	AGACACCGGT	2100
CTGCTGTGCG	TATATCGGCA	TCAGCTTTCT	CGACAGGCTC	AGTCAACGGG	GACTCGGCTA	2160
GGCGCAACTA	GGCAATAGCT	CTGCGAATTT	CTTGTTCGCG	GACCGCGAAA	GCATTCAGGC	2220
CGGCGCGGCT	GGTTTGGCAT	CGAAAACTCC	GGCGAACCGA	GGGATTTCGA	TGCTCGACGG	2280
GGCGCGCTCG	GACGCGTATC	CGATCATCAA	CTACGAGTAC	CGCATTCCTA	ACACACGGCA	2340
AAAGGACGCC	CGCACCGCGC	AGACTTTGCA	GGCATTTCCT	CATGCGGCGA	TACCGGACCG	2400
CACCAAGGCG	TGCTTGTCTG	ACCAAGTTCA	TTTCGAGCGG	CTGCGCGCGG	CGGTGCTGAA	2460
GCTGCTGAGC	GGCTTTGATC	CGACGATTTT	CAGCGCTGAG	ATGAGAGCGG	ATGCGCTCAT	2520
CGCTCGCGCG	GAGGCAGGTA	ATTTCGAGCG	GATCTCCGCG	GACTTCGAAA	CCGAGATCGA	2580
CGAGCTGAGG	TGACGCGGAG	GTTCCTTGCA	GGGCGAGTGG	CGCGCGCGCG	CGGCGACCGC	2640
CGCGCGCGCG	CGCGCTGTGC	GCTTCGAGGA	AGCGCGCAAT	AAGCAGAAAG	AGGAAGCTCGA	2700
CGAGATCTCG	ACGAATATTC	GTCAAGGCGG	CGTCCAAATC	TGAGGGGCGG	ACGAGGAGCG	2760
CGAGCAGGCG	CTGTCCTGCG	AAATGGGCTT	TGGATTTCAG	TTGCGCTGCG	CTGCTGCTGT	2820
GGTGGAGTGT	GAGCGCGCGC	ACTTCGAGTA	CGGTTTCAGCA	CTGCTTCAGCA	AAACCAACCGG	2880
GGAGCTCGCA	TTTCCCGGAC	AGCGCGCGCG	GGTGCGCATC	GACACCGGTA	TGCTGTCTCG	2940
CGGCTTAGAC	TAAAGGCTTT	ACGCTAGGCG	CGAAGCGCAC	GACTCGAAGG	CGCGCGCGCG	3000
GTTTGGGCTG	GACATGGGTT	AGTTTATAT	GGCTTACCGG	GGCACCCGGA	TCAACTAGGA	3060

AACCGTCTCG	CTYGACGCCA	ACGGGGTGTC	TGGAAGCGCG	TCGTATTACG	AAGTCAAGTT	3120
CAGCGATCCG	AGTAAGCCGA	ACGGCCAGAT	CTGGACGGGC	GTATCGGCT	CGCCCGCGGC	3180
GAACGCCACG	GACGCGGGC	CCCTCAGCG	CTGGTTTGTG	GTATGCTCG	GGACCGCCAA	3240
CAACCGGGTG	GACAAGGGCG	CGGCCAAGGC	GCTGGCCGAA	TGGATCGGGC	CTTTGGGTGG	3300
CCCGCGCGCG	GGCTGGCGCG	GGGAGTGGC	TCTTACCCCG	ACGACACCGA	CACCCGAGCG	3360
GACCTTACCG	GGCTGAGAA	TCTGACGATA	TCCATCACAC	TGGCGCGCGC	TGGAGCACCA	3420
CCACCCACCAC	CACCTGAGATC	CGGCTGCTAA	CRAAGCCCGA	AAGGAAGCTG	AGTTGGCTGC	3480
TGCCACCGCT	GAGCAATAAC	TAGCATAACC	CCTTGGGGCC	TCTAAGCGGG	TCTTGGGGGG	3540
TTTTTTCGCT	AAAGGAGGAA	CTATATCCGG	AT			3572

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Val	Gln	Phe	Gln	Ser	Gly	Gly	Asp	Asn	Ser	Pro	Ala	Val	Tyr	Xaa	Xaa
1			5					10						15	
Asp	Gly	Xaa	Arg												20

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Thr	Thr	Val	Pro	Xaa	Val	Thr	Glu	Ala	Arg
1			5				10		

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Thr	Thr	Pro	Ser	Xaa	Val	Ala	Phe	Ala	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

269

1 5 10

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Asp Ala Gly Lys Xaa Ala Gly Xaa Asp Val Xaa Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Thr Xaa Glu Glu Xaa Gln Glu Ser Phe Asn Ser Ala Ala Pro Gly Asn
 1 5 10 15
 Xaa Lys

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CTAGTATGTA CTCATCTCCA GACCGTG

27

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GCGATGACCA ATTCACTTCG ACTCC

25

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

CATATGGGCC	ATCATCATCA	TCATCACGTC	ATCGACATCA	TCGGGACACC	CCCCAGATCC	60
TGGGAACACG	CGGCGGCGGA	GGCGGTCGAG	CGGGCGCGGG	ATAGCGTCGA	TGACATCCGC	120
GTGCTGTCGG	TCATTNAGCA	GGACATGGCC	GTGGACAGCG	CGCGCAAGAT	CACCTACGCG	180
ATCAAGGCTG	AAGTGTGCTT	CAAGATGAGG	CGGGCGCAAC	CGAGGGGGCTC	GAACCCACCG	240
AGCGGTTCCG	CTGAAGAGGG	CGCGCGCGCC	GGTACTCTCG	CGACTACCCC	CGCGTGGTCG	300
CGGTTGACTT	TGGCGGAGAC	CGGTAGCAGC	CTGCTCTACC	CGCTGTTCAA	CGTGTGGGGT	360
CGGCGCTTTC	ACGAGAGGTA	TCCGAACGTC	ACGATCACCG	CTCAGGGGAC	CGGTTCTGGT	420
CGCGGGATCG	CGCAGGCGCG	CGCGGGGACG	GTCAACATTG	CGGCTTCCGA	CGCCTATCTG	480
TGGGAAGGTC	ATATGGCGCG	GCACAAGGGG	CTGATGAACA	TCGCGCTAGC	CATCTCGCGT	540
CAGCAGGTCA	ACTACCACTT	CGCGGGAGTG	AGCGAGCACC	TCAAGCTGAA	CGGAAAAGTC	600
CTGGCGGGCA	TGTACGAGGG	CACCA TCAAA	ACCTGGGACG	ACCGGTCAGT	CGCTTGCCTC	660
AACCGCGGCG	TGAACCTGCT	CGGCAACGGC	GTAGTTCCCG	TGCACCGGCTC	CGACGGGTCC	720
GGTGACACTT	TCTTTGTCAG	CGAGTACCTG	TCCAGCAAG	ATCCCGAAGG	CTGGGGCAAG	780
TGCGCCGCGT	TGGGCAACGC	CGCTGACTTC	CGGCGGCTGC	CGGTTGCTCT	GGGTGAGAAC	840
GGCAACGGCG	GCATGGTGAC	CGTTGCGCGC	GAGACACCGG	CGTGGCTTGG	CTATATCGGC	900
ATCAGCTTTC	TGGACGAGCG	CAGTCAACGG	GGACTCGGCG	AGGCCCAACT	AGGCAATAGC	960
TCTGGCAATT	TCTTTGTCGC	CGACCGCGCA	AGCAATTCAG	CGCGGGCGGG	TGGCTTCCCA	1020
TGGAAGACGC	CGGCGAACCA	GGCGATTTCG	ATGATCGAGC	GGCGCGCGCC	GGACGGCTAC	1080
CGGATCATCA	ACTACGAGTA	CGCATCGCTC	AACCAACCGC	AAAGGAGCGC	CGCCACCGCG	1140
CAGACCTTTC	AGGCATTTCT	CGACTGGGCG	ATCACCGGAC	GCAACAAGCG	CTCTTCTCTC	1200
GACCAGGCTC	ATTTCGAGCG	GCTCGCGGCG	CGGGTGGTGA	AGTTTGTCTG	CGCTTGTGTC	1260
CGGACGATTT	CGAGCGCTGA	GATGAAGAGC	GATCGCGCTA	CGCTCGCGCA	GGAGGCAAGT	1320
AATTTGCGAG	GGATCTCCGG	CGACCTGAAA	ACCCAGATCG	ACCAGGTGGA	GTCCAGCGCA	1380
GGTTCTGTCG	AGGGCGAGTG	CGCGGGCGCG	CGGGGAGCGG	CGGCGCAGGG	CGCGGTGGTG	1440
CGCTTCAAG	AAGCAGCCAA	TAAGCAGAAG	CAGGAACCTG	ACGAGATCTC	GACGAATATT	1500
CGTCAGGCGC	GGCTGCAATA	CTCGAGGGCC	SACGAGGAGC	AGCAGCTAGC	GGTCTCTCTG	1560
CAATGGGCTT	TGTGCGCCAC	AACGGCGGCG	TGCGCGCGCT	CGACCGCTGC	AGCGCCACCG	1620
CGACTCGGCG	CACCTGTTCG	CGCCGCACTA	CGCCCGGCGG	CGAACACGCG	GAATGCCGAG	1680
CGGCGGCGAT	CGACCGCAGC	ACCTCTCGCG	CGCGACCGGA	ACGCACTGCG	CGCACTTGTG	1740
ATTGCGCCAA	ACGCAAGCCAA	ACCTGTGCGG	ATGACCAACC	CGGTTGGAGG	ATTGACTCTC	1800
CGCGTGGCTG	TGGCTGGGCT	GGAGTCTGAC	CGCCCGCACT	TGCACTACGG	TTGCGCACTC	1860
CTCAGCAAAA	CGACCGGGGA	CGCGGCATT	CGCGGACAGC	CGCGCGCGGT	GGCCCAATGAC	1920
TGCTCTATGC	TGCTGTGTCG	GCTAGACCAA	AAGCTTTTAC	CGAGCGCGGA	AGCCACCGAG	1980
TCCAGGGGCG	CGGCGCGGTT	GGGCTCGGAC	ATGGGTGAGT	TCTATATGCG	CTACCGGGCG	2040
ACCGGAGTCA	ACCGGAGAAC	CGCTCGCTTC	GACGCCAAGC	GGGTGTCTGG	AAGCGCGTGC	2100
TATTACGAAG	TCAAGTTTCG	CGATCGGAGT	AAGCCGAAGC	GCCAGATCTG	GACGCGCGTA	2160

ATCGGCTGCG	CCGCGGCGAA	CGCACCGGAC	GCCTGGGCCC	CTCAGCGCTG	GTTTGTGGTA	2.20
TGCGCTCGGA	CCGCGCAACA	CCCGGTGGAC	CAAGGCGCGC	CCAAGCTCTT	GGCGCAATCC	2.26
ATCGCGCGTT	TGGTGGCCGC	CCGCGGCGCG	CACCGACCGG	CTCTGCGAGT	GGCGGCTGCG	2.340
GCACCGCGCG	CGGCGGGGGA	AGTCGCTCTT	ACCCGACGSA	CACCGACCGC	GCAGCGGACC	2.400
TTACCGCTCT	GA					2.422

(2) INFORMATION FOR SEC ID NO: 351:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: PROTEIN

[41] SEQUENCE DESCRIPTION: GPO TO NO: 251.

Met	Gly	His	His	His	His	His	His	Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser
1			5						10					15	
Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala	Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg
			20					25					30		
Asp	Ser	Val	Asp	Asp	Ile	Arg	Val	Ala	Arg	Val	Ile	Glu	Gln	Asp	Met
		35					40					45			
Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile	Thr	Tyr	Arg	Ile	Lys	Leu	Glu	Val
		50				55					60				
Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln	Pro	Arg	Gly	Ser	Lys	Pro	Pro	Ser
65				70					75					80	
Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro
				85					90					95	
Ala	Set	Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr
			100					105					110		
Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Tyr	Pro
			115			120						125			
Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln
			130			135					140				
Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser
145				150					155					160	
Glu	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala
			165					170						175	
Ile	Ser	Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His
			180					185					190		
Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile
		195				200						205			
Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn
		210				215						220			
Leu	Pro	Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly
225				230					235					240	
Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly
			245					250						255	
Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val
			260					265					270		
Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys
		275				280						285			
Ala	Gln	Thr	Pro	Glu	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp

290	295	300
Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser		
305	310	315
Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala		320
	325	330
Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp		335
	340	345
Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile		350
	355	360
Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala		365
	370	375
Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp		380
	385	390
Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp		395
	405	410
Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala		415
	420	425
Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu		430
	435	440
Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly		445
	450	455
Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg		460
	465	470
Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser		475
	485	490
Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu		495
	500	505
Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala		510
	515	520
Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro		525
	530	535
Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro		540
	545	550
Gly Asp Pro Asn Ala Ala Pro Pro Ala Asp Pro Asn Ala Pro Pro		555
	565	570
Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn		575
	580	585
Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser		590
	595	600
Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr		605
	610	615
Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr		620
	625	630
Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu		635
	645	650
Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu		655
	660	665
Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser		670
	675	680
Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys		685
	690	695
Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile		700
	705	710
Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp		715
	725	730
		735

Phe	Val	Val	Trp	Leu	Gly	Thr	Ala	Asn	Asp	Pro	Val	Asp	Lys	Gly	Ala
			740					745						750	
Ala	Lys	Ala	Leu	Ala	Glu	Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Pro
		755					760					765			
Ala	Pro	Ala	Pro	Ala	Pro	Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala
	770				775						780				
Gly	Glu	Val	Ala	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu
	785				790					795					800
Pro	Ala														

(12) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GGATCCAAAC CACCGAGCGG TTCGCTGAA ACGG

34

(12) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CGCTCGAAT TCACCTCGG AGGAATCGT CGCGATC

37

(12) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

CATATGGGCC	ATCATCATCA	TCATCAGGA	TCCAAACCAC	CGAGCGGTTT	GCTTGAACG	60
GGCGCCGCG	CCGCTACTGT	CGGCTACTCC	CCGCGTGTGT	CGCCGGTGAC	GTTCGCGGAG	120
ACGGTAGCA	CGCTGCTCA	CCGCTGTTC	AACCTGTGG	GTCCGGCTTT	TCACGAGAG	180
TATCCGAAC	TCACGATCAC	CGCTCAGGG	ACGGTTTCT	GTCCGGGGAT	CGCGCAGGCC	240

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GCCGCCGGGA CGGTCAACAT TCGGGCCTCC GACGCCATC TGTGGGAAGG TGATATGGCC 300
GGCACAAGG GCGTATGAA CATCGCGCTA GCGCTCTCG CTGAGCAGGT GAATACCAAC 350
CTGCCCGGAG TGAGCGAGCA CCTCAAGCTG AACGGAAAG TCTGGCGGC CATGTACCAG 420
GGCACCATCA AAAGCTGGGA CGACCCGCG AGTCGTGGC TCAACCCCGG CTTGAACCTG 480
CCCGGCACCG CGGTAGTTCC GCTGCACCGC TCGGACGGGT CGGTGACAC CTTCCTGTTT 540
ACCGATACG TGTCAAGCA AGATCCCGAG GCGTGGGGCA AGTGCCTCG CTTGGGCACC 600
ACCGTCGACT TCCCGGCGGT GCGGGGTGCG CTGGGTGAGA ACGGCAACGG CGGCATGGTG 660
ACCGGTTGCG CCGAGACAC GGGCTGCGT GCGTATATCG GCATCAGCTT CCTCGACCTG 720
GCCAGTCAAC GGGAGCTCGG CGAGGCCCAA CTAGGCAATA GCTCTGGCAA TTCTTGTTG 780
CCCGACCGCG AAAGCATTCG GCGCGCGCGG CTTGGCTTCG CATCGAAAAC CCGCGCGAAC 840
CGGGCGATTT CGATGATCGA GCGGCGCGCG CCGGACGGCT ACCGATCAT CAATACGAG 900
TAGCGCATCG TCAACACCG GCAAAAGGAC GCGGCCACCG CGCAGACCTT CGAGGCATTT 960
CTGCACTAGG CATCACCGA CGGCAACAG GCGTCTGTC TCGACAGGT TCATTTCCAG 1020
CGCTGCGCG CCGCGGTGCT GAAGTTGCT GACGCGTTGA TCGCGACGAT TTCTTCGGA 1080
GGTGGCAGTG GGGGAGGCT AGGTGGAGGT TCTGGCGGGA GCGTGGCCAC AACCGCGCGC 1140
TCCGCGCGCT CGAGCGCTCG AGCGCGAGCG GCACCGCGGA CACTGTTTCG CCGCGCGAGC 1200
CGCGCGCGCG CCAACAGCG GATGCGCG CCGGGCATC CCAACGCGAG ACCTTCGCGC 1260
CGCGACCGGA CGCGCGCGCG GCCACCTGTC ATTCGCGCA ACGCACCGCA ACCTTCGCGC 1320
ATCGACAAC CGGTGAGAG ATTGAGCTTC GCGCTGCTTC CTGCGTGGGT GAGTCTGAC 1380
CGCGCGCGCT TCGACTACGG TTCAGCACT CTCAGCAAAA CCACCGCGGA CCGCGCATTT 1440
CGCGACCGCG CGCGCGCGCT GCGCAATGAC ACCGCTATCG TCGTGGCGGC CTGAGACCAA 1500
AAGCTTTAGC CGACCGCGGA AGCCACCGAG TCCAGGGCG CGCGCGGTT GCGCTCGGAC 1560
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GACCGCAACG GCGTGTCTCG AAGCGCGTTC TATTAGGAG TCAAGTTTCA CGATCCGAGT 1680
AAGCGCAACG GCGGATCTG GACCGCGCTA ATCGCTGCG CCGCGCGGAA CCGACCGGAG 1740
CGCGCGCGCG CTCAGCGCTG GTTGTGTTA TGGTGGGGA CCGCGCAACA CCGGTGGAGC 1800
AAGCGCGCG CCAAGCGCGT GCGCGAATCG ATCGCGCTT TGGTGGCGCG CCGCGCGCGC 1860
CGCGCACCGG CTCTGAGGA GCGCGCTCG GCGCGCGCG CCGCGCGGGA AGTGGCTCT 1920
ACCGCGAGCA CACCGACACC GCAGCGGACT TTACCGCGCT GA 1962

```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 amino acids
- (B) TYPE: amino acid
- (C) STRADEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:355:

```

Met Gly His His His His His Gly Ser Lys Pro Pro Ser Gly Ser
1      5      10      15
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
20      25      30
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
35      40      45
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
50      55      60
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
65      70      75      80
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
85      90      95
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser

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100 105 110
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 115 120 125
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 130 135 140
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 145 150 155 160
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 165 170 175
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 180 185 190
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 195 200 205
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 210 215 220
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 225 230 235 240
 Ser Gln Arg Gly Leu Gly Gln Ala Gln Leu Gly Asn Ser Ser Gly Asn
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 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
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 275 280 285
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 290 295 300
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 305 310 315 320
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 325 330 335
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
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 Ile Ala Thr Ile Ser Ser Gly Gly Gly Gly Gly Ser Gly Gly
 355 360 365
 Gly Ser Gly Gly Ser Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 370 375 380
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 385 390 395 400
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 405 410 415
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Val Ile Ala Pro
 420 425 430
 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
 435 440 445
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
 450 455 460
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
 465 470 475 480
 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
 485 490 495
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
 500 505 510
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 515 520 525
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 530 535 540

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Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn	
565	570 575
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly	
580	585 590
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu	
595	600 605
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro	
610	615 620
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr	
625	630 635 640
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala	
645	650

CLAIMS

1. A polypeptide comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu; (SEQ ID No. 120)
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser; (SEQ ID No. 121)
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 122)
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro; (SEQ ID No. 123)
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val; (SEQ ID No. 124)
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID No. 125)
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser; (SEQ ID No. 126)
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly; (SEQ ID No. 127)
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn; (SEQ ID No. 128) and
- (j) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136)

wherein Xaa may be any amino acid.

2. A polypeptide comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative

substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID No. 129) and
- (b) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No. 137), wherein Xaa may be any amino acid.

3. A polypeptide comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101 or a complement thereof under moderately stringent conditions.

4. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 26-51, 138, 139, 163-183, 201, 240, 242-247, 253-256, 295-298, 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 26-51, 138, 139, 163-183, 201, 240, 242-247, 253-256, 295-298, 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341 or a complement thereof under moderately stringent conditions.

5. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1-4,

6. An expression vector comprising a DNA molecule according to claim 5.

7. A host cell transformed with an expression vector according to claim 6.
8. The host cell of claim 7 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
9. A pharmaceutical composition comprising one or more polypeptides according to any one of claims 1-4 and a physiologically acceptable carrier.
10. A pharmaceutical composition comprising one or more DNA molecules according to claim 5 and a physiologically acceptable carrier.
11. A pharmaceutical composition comprising one or more DNA sequences recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and a physiologically acceptable carrier.
12. A vaccine comprising one or more polypeptides according to any one of claims 1-4 and a non-specific immune response enhancer.
13. A vaccine comprising:
 - a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and
 - a non-specific immune response enhancer.
14. A vaccine comprising:
 - one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and

a non-specific immune response enhancer.

15. The vaccine of claims 12-14 wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine comprising one or more DNA molecules according to claim 5 and a non-specific immune response enhancer.

17. A vaccine comprising one or more DNA sequences recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and a non-specific immune response enhancer.

18. The vaccine of claims 16 or 17 wherein the non-specific immune response enhancer is an adjuvant.

19. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to any one of claims 9-11.

20. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 12-18.

21. A fusion protein comprising two or more polypeptides according to any one of claims 1-4.

22. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and ESAT-6.

23. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and the *M. tuberculosis* antigen 38 kD (SEQ ID NO:155).

24. A pharmaceutical composition comprising a fusion protein according to any one of claims 21-23 and a physiologically acceptable carrier.

25. A vaccine comprising a fusion protein according to any one of claims 21-23 and a non-specific immune response enhancer.

26. The vaccine of claim 25 wherein the non-specific immune response enhancer is an adjuvant.

27. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to claim 24.

28. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to claims 25 or 26.

29. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with one or more polypeptides according to any one of claims 1-4; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

30. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

31. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308,

310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

32. The method of any one of claims 29-31 wherein the immune response is induration.

33. A diagnostic kit comprising:

- (a) a polypeptide according to any one of claims 1-4; and
- (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

34. A diagnostic kit comprising:

- (a) a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and
- (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

35. A diagnostic kit comprising:

- (a) a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and
- (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

36. A diagnostic kit comprising:

- (a) a fusion protein according to any one of claims 21-23; and
- (b) apparatus sufficient to contact said fusion protein with the dermal cells of a patient.

37. A fusion protein according to claim 23 comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 153, 209, 351 and 355.

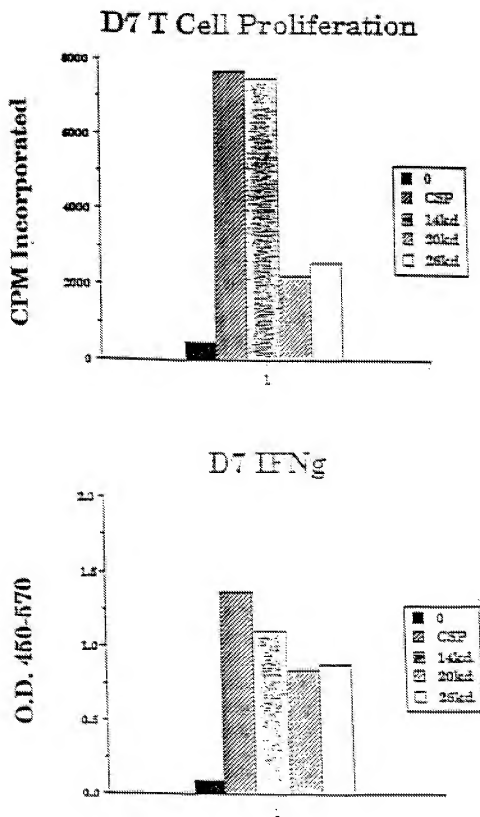


FIG. 12

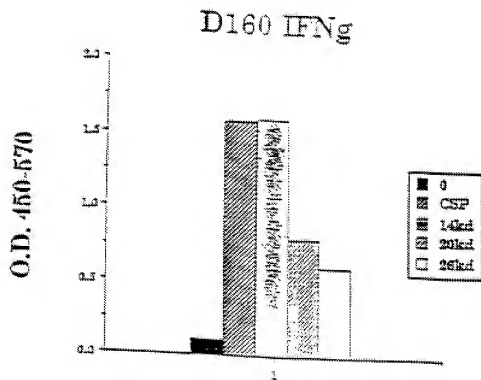
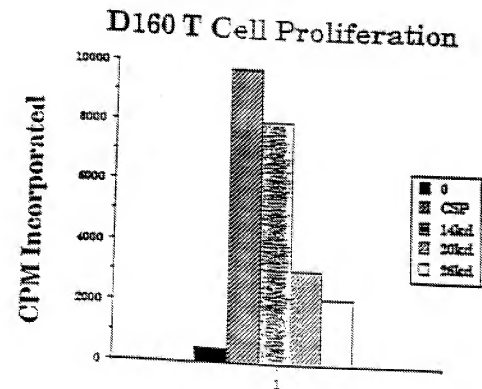


FIG. 1B

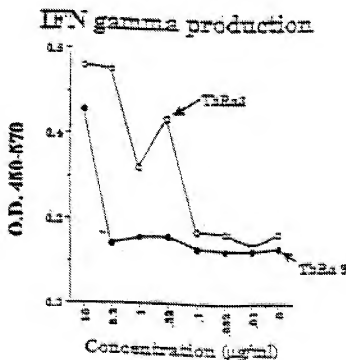
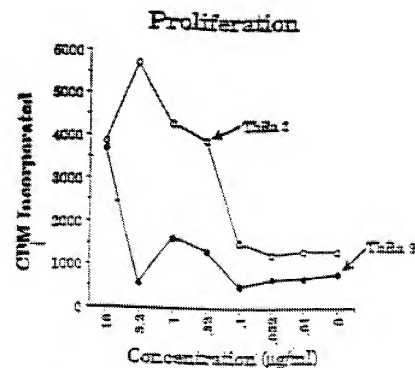
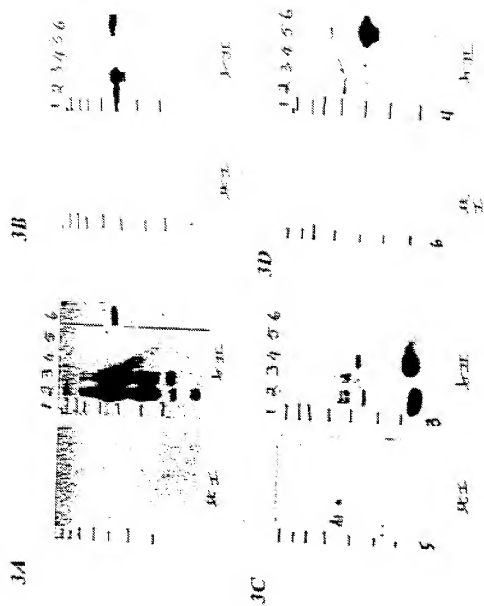


FIG. 2



FIGS. 3A-D

T cell clone 131TbH9 responds poorly to CSP

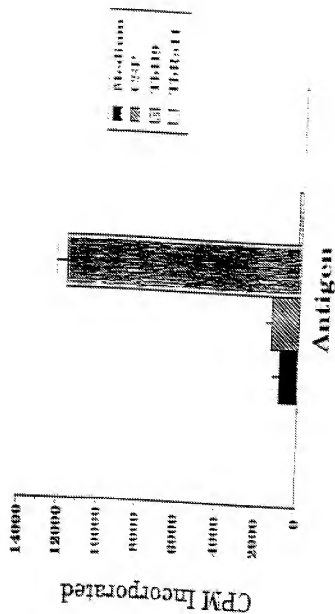


FIG. 4A

T Cell Clone PPD 800-10 IFN γ Production

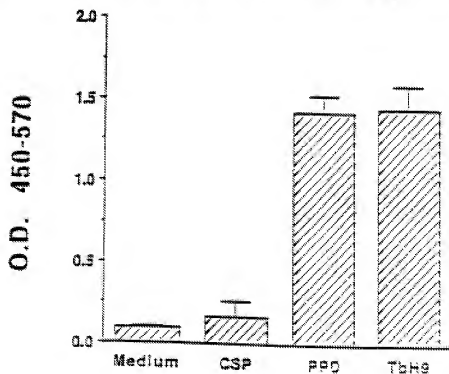
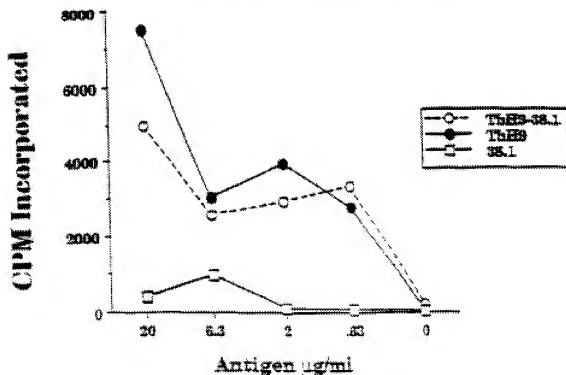
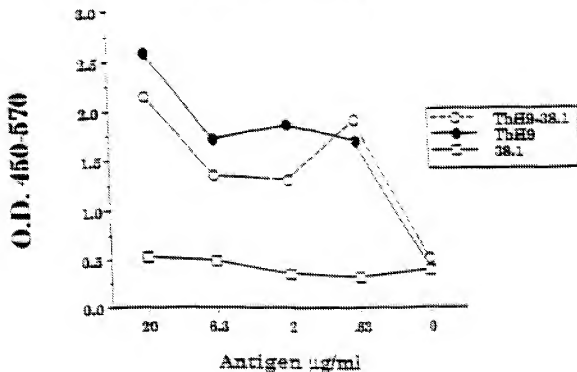


FIG. 4B

D131 T Cell Proliferation

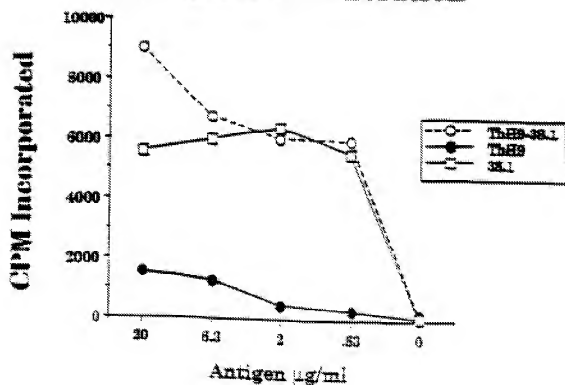


D131 IFN γ

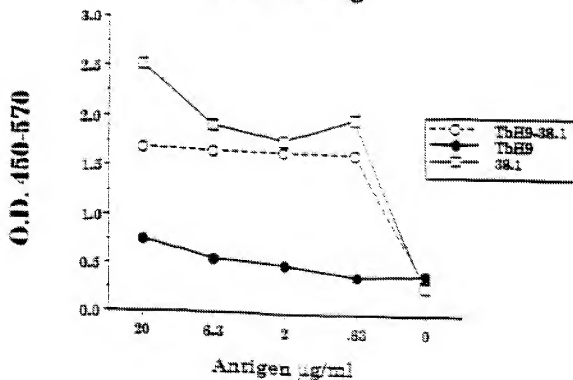


FIGS. 5 A-B

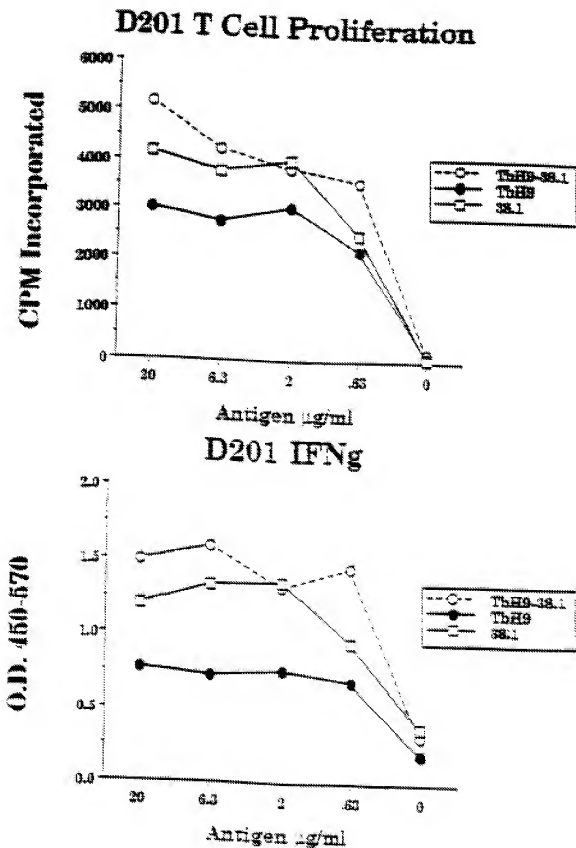
D184 T Cell Proliferation



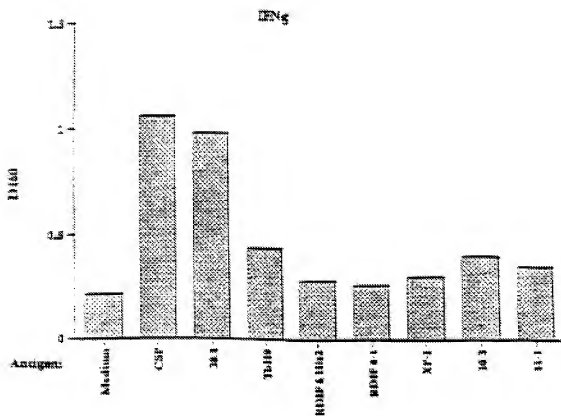
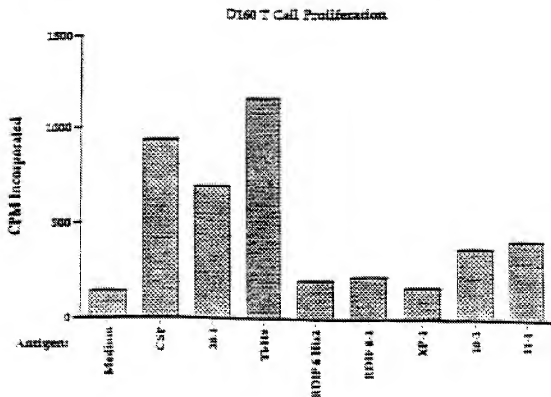
D184 IFN γ



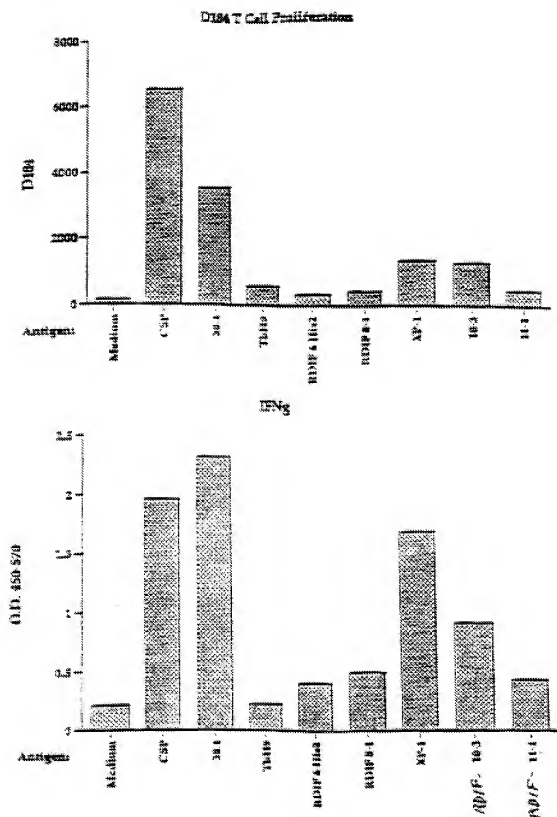
FIGS. 6 A-B



FIGS. 7 A-B



FIGS. 8A-B



FIGS. 9A-B

**Tuberculosis: Protection of Cynomolgus Monkeys
with Recombinant Antigens of Mtb**

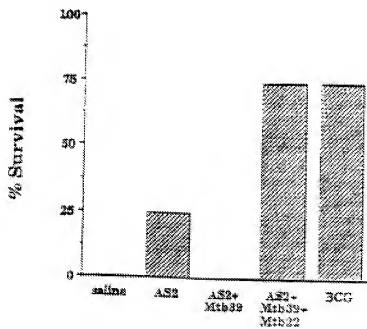
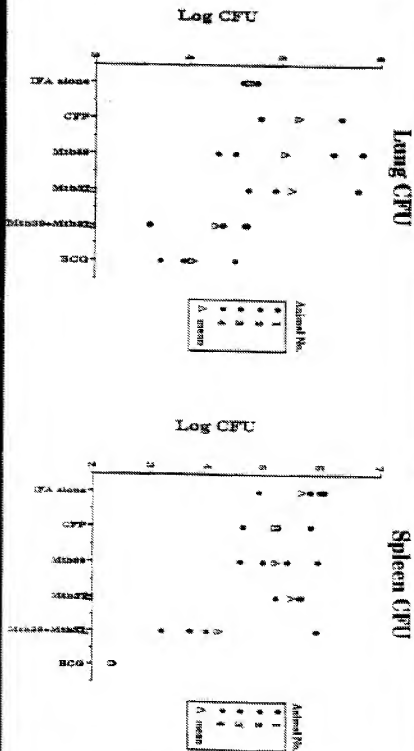


FIG. 10

Aerosol TB Challenge of Vaccinated Guinea Pigs



FIGS. 11 A-B

**DNA Immunized mice challenged
with aerosol TB (lung CFU)**

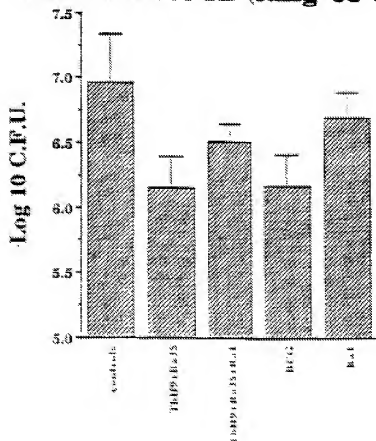


FIG. 12